

SEQUENCE LISTING

<110> Kroger, Burkhard
Zelder, Oskar
Kolpprogge, Corinna
Schroder, Hartwig
Hafner, Stefan

<120> Method for Zymotic Production of Fine Chemicals Containing
Sulphur (Meta)

<130> 13111-00002-US

<150> PCT/EP 2003/009452

<151> 2003-08-26

<150> DE 102 39 073.8

<151> 2002-08-26

<160> 69

<170> PatentIn version 3.3

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<222> (1)..(1101)

<223> RDI00386

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<213> Corynebacterium diptheriae

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Pro Gly Lys Ala Leu Asp Thr Asn Arg Tyr Cys Ile Leu Cys Thr Asn
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Ser Gly His Ala Pro Trp Glu Gly Ile Ala Ala Ala Arg Arg Ile Ala
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His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg Phe Gly Thr
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Ser Ala Gln His Gly Glu Asn Pro Leu Gly Pro Phe Arg Asp Pro His

225 230 235 240
 Gln Arg Phe Ala Val Thr Ser Tyr Leu Gln His Gln Gly Ile Lys Leu
 245 250 255
 Ala Gln Arg Phe Asp Ala Gly Ser Tyr Val Val Leu Thr Glu Ala Leu
 260 265 270
 Asn Arg His Asp Ile Gly Arg Gly Arg Gly Gly Leu Asn Lys Ala Leu
 275 280 285
 Ser Ala Ile Thr Val Pro Ile Met Ile Ala Gly Val Asp Thr Asp Ile
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 Leu Leu Ala Met Ala Lys Ile Ser Ser Pro Val Gly His Asp Ala Phe
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<223> RML02951

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Asp Trp Ile Ala Gly Pro Gly Ala Pro Ile Asp Thr Asn Arg Trp Cys	
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Ala Ile Ala Thr Asn Val Leu Gly Gly Cys Arg Gly Ser Thr Gly Pro	
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<213> Mycobacterium tuberculosis

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 65 70 75 80

Asp Gly Val Ala Gly Pro Ser Ala Pro Ile Asp Thr Thr Arg Trp Cys
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Ser Ser Leu Ala Arg Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Leu
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 195 200 205

Ser Gly Asp Tyr His Glu Thr Gly Arg Ala Pro Asp Ala Gly Leu Arg
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Leu Ala Arg Arg Phe Ala His Leu Thr Tyr Arg Gly Glu Ile Glu Leu
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<223> RCL01447

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195 200 205	

ttc gaa gcc gaa agc tac gtg cgt cac cag ggc gac aag ctg gtt ggg 672
 Phe Glu Ala Glu Ser Tyr Val Arg His Gln Gly Asp Lys Leu Val Gly
 210 215 220
 cgc ttt gat gca aac acc tat atc acg ctc acc aga gcg atg gac atg 720
 Arg Phe Asp Ala Asn Thr Tyr Ile Thr Leu Thr Arg Ala Met Asp Met
 225 230 235 240
 cac gac ctc ggg cgc gga cgc gac tcc tac gaa gcg gcg ctc gga gcg 768
 His Asp Leu Gly Arg Gly Arg Asp Ser Tyr Glu Ala Ala Leu Gly Ala
 245 250 255
 ctg aag atg ccg gtc gag att ctc tcc atc gac tcg gac gtg ctc tat 816
 Leu Lys Met Pro Val Glu Ile Leu Ser Ile Asp Ser Asp Val Leu Tyr
 260 265 270
 ccc agg cag gag cag gag gaa ctt gcc cgc ctc att ccc ggc tca cgc 864
 Pro Arg Gln Glu Gln Glu Glu Ala Arg Leu Ile Pro Gly Ser Arg
 275 280 285
 ctg ctt ttc ctt gac gaa ccc tat ggc cac gac gcc ttt ctt atc gac 912
 Leu Leu Phe Leu Asp Glu Pro Tyr Gly His Asp Ala Phe Leu Ile Asp
 290 295 300
 acc gag acc gtc agc cgc atg gtc tgc gag ttc aag agg cag ttg ata 960
 Thr Glu Thr Val Ser Arg Met Val Cys Glu Phe Lys Arg Gln Leu Ile
 305 310 315 320
 gtt gac aat tga 972
 Val Asp Asn

<210> 8
 <211> 323
 <212> PRT
 <213> Chlorobium tepidum

<400> 8
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 Ser Trp Trp Cys Gly Met Phe Gly Glu Gly Arg Ala Phe Asp Glu Thr
 35 40 45
 Arg Asp Phe Ile Val Cys Ser Asn Val Leu Gly Ser Cys Tyr Gly Thr
 50 55 60
 Thr Gly Pro Met Ser Val Asn Pro Leu Ser Gly Arg His Tyr Gly Pro
 65 70 75 80
 Asp Phe Pro Arg Ile Thr Ile Arg Asp Met Val Asn Val Gln Arg Leu
 85 90 95
 Leu Leu Arg Ser Leu Gly Ile Asp Arg Ile Arg Leu Ile Val Gly Ala

100

105

110

Ser Leu Gly Gly Met Gln Val Leu Glu Trp Gly Ala Met Tyr Pro Glu
115 120 125

Met Ala Gly Ala Leu Met Pro Met Gly Val Ser Gly Arg His Ser Ala
130 135 140

Trp Cys Ile Ala Gln Ser Glu Ala Gln Arg Gln Ala Ile Ala Ala Asp
145 150 155 160

Ala Glu Trp Gln Asp Gly Trp Tyr Asp Pro Glu Val Gln Pro Arg Lys
165 170 175

Gly Leu Ala Ala Ala Arg Met Met Ala Met Cys Thr Tyr Arg Cys Phe
180 185 190

Glu Asn Tyr Gln Gln Arg Phe Gly Arg Lys Gln Arg Glu Asp Gly Leu
195 200 205

Phe Glu Ala Glu Ser Tyr Val Arg His Gln Gly Asp Lys Leu Val Gly
210 215 220

Arg Phe Asp Ala Asn Thr Tyr Ile Thr Leu Thr Arg Ala Met Asp Met
225 230 235 240

His Asp Leu Gly Arg Gly Arg Asp Ser Tyr Glu Ala Ala Leu Gly Ala
245 250 255

Leu Lys Met Pro Val Glu Ile Leu Ser Ile Asp Ser Asp Val Leu Tyr
260 265 270

Pro Arg Gln Glu Gln Glu Glu Leu Ala Arg Leu Ile Pro Gly Ser Arg
275 280 285

Leu Leu Phe Leu Asp Glu Pro Tyr Gly His Asp Ala Phe Leu Ile Asp
290 295 300

Thr Glu Thr Val Ser Arg Met Val Cys Glu Phe Lys Arg Gln Leu Ile
305 310 315 320

Val Asp Asn

<210> 9

<211> 1149

<212> DNA

<213> *Caulobacter crescentus*

<220>

<221> CDS

<222> (1)..(1146)

<223> RCO00727

<400> 9

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ttt cct gcg aat gaa cct ctg cgg ctg gac tcc gga ggc gtc atc gaa	96
Phe Pro Ala Asn Glu Pro Leu Arg Leu Asp Ser Gly Gly Val Ile Glu	
20 25 30	
ggt ctg gaa atc gcc tac cag acc tac ggc cag ctg aac gcg gac aag	144
Gly Leu Glu Ile Ala Tyr Gln Thr Tyr Gly Gln Leu Asn Ala Asp Lys	
35 40 45	
tcc aac gcc gtc ctg atc tgc cac gcc ctg acg ggc gac cag cat gtg	192
Ser Asn Ala Val Leu Ile Cys His Ala Leu Thr Gly Asp Gln His Val	
50 55 60	
gcc tcg ccc cac ccc acc acc ggc aag ccc ggc tgg tgg caa cgc ctt	240
Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu	
65 70 75 80	
gtt ggt ccc ggt aag ccg ctg gat ccc gcg cgg cac ttc atc atc tgc	288
Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys	
85 90 95	
tcg aac gtg atc ggc ggc tgc atg ggc tcg acg ggc ccg gcc tcg atc	336
Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile	
100 105 110	
aat ccg gcc acg ggc aag acc tat ggc ctg tcg ttc cca gtc atc acc	384
Asn Pro Ala Thr Gly Lys Thr Tyr Gly Leu Ser Phe Pro Val Ile Thr	
115 120 125	
atc gcc gat atg gtg cgg gcc cag gcc atg ctg gtc tct gcg ctc ggg	432
Ile Ala Asp Met Val Arg Ala Gln Ala Met Leu Val Ser Ala Leu Gly	
130 135 140	
gtc gag acc ctg ttc gcc gtc gtc ggc ggc tcg atg ggc ggc atg cag	480
Val Glu Thr Leu Phe Ala Val Val Gly Gly Ser Met Gly Gly Met Gln	
145 150 155 160	
gtc cag caa tgg gcc gtg gac tat ccc gag cgg atg ttc agc gcc gtg	528
Val Gln Gln Trp Ala Val Asp Tyr Pro Glu Arg Met Phe Ser Ala Val	
165 170 175	
gtg ctg gcc tcg gcc tcg cgc cac tcg gcc cag aac atc gcg ttc cac	576
Val Leu Ala Ser Ala Ser Arg His Ser Ala Gln Asn Ile Ala Phe His	
180 185 190	
gag gtg ggc cgc cag gcg atc atg gcc gat ccc gac tgg cgc ggc ggc	624
Glu Val Gly Arg Gln Ala Ile Met Ala Asp Pro Asp Trp Arg Gly Gly	
195 200 205	
gcc tat gcc gag cac ggc gtg cgg ccc gag aag ggc ctg gcc gtg gcg	672
Ala Tyr Ala Glu His Gly Val Arg Pro Glu Lys Gly Leu Ala Val Ala	
210 215 220	
cgg atg gcc gcg cac atc acc tat ctg tcc gag ccc gcc ctg cag cgg	720
Arg Met Ala Ala His Ile Thr Tyr Leu Ser Glu Pro Ala Leu Gln Arg	
225 230 235 240	
aag ttc ggc cgc gag cta cag cgc gac ggc ctc tcc tgg ggc ttt gac	768
Lys Phe Gly Arg Glu Leu Gln Arg Asp Gly Leu Ser Trp Gly Phe Asp	
245 250 255	

100	105	110
Asn Pro Ala Thr Gly Lys Thr Tyr Gly Leu Ser Phe Pro Val Ile Thr 115 120 125		
Ile Ala Asp Met Val Arg Ala Gln Ala Met Leu Val Ser Ala Leu Gly 130 135 140		
Val Glu Thr Leu Phe Ala Val Val Gly Gly Ser Met Gly Gly Met Gln 145 150 155 160		
Val Gln Gln Trp Ala Val Asp Tyr Pro Glu Arg Met Phe Ser Ala Val 165 170 175		
Val Leu Ala Ser Ala Ser Arg His Ser Ala Gln Asn Ile Ala Phe His 180 185 190		
Glu Val Gly Arg Gln Ala Ile Met Ala Asp Pro Asp Trp Arg Gly Gly 195 200 205		
Ala Tyr Ala Glu His Gly Val Arg Pro Glu Lys Gly Leu Ala Val Ala 210 215 220		
Arg Met Ala Ala His Ile Thr Tyr Leu Ser Glu Pro Ala Leu Gln Arg 225 230 235 240		
Lys Phe Gly Arg Glu Leu Gln Arg Asp Gly Leu Ser Trp Gly Phe Asp 245 250 255		
Ala Asp Phe Gln Val Glu Ser Tyr Leu Arg His Gln Gly Ser Ser Phe 260 265 270		
Val Asp Arg Phe Asp Ala Asn Ser Tyr Leu Tyr Ile Thr Arg Ala Met 275 280 285		
Asp Tyr Phe Asp Ile Ala Ala Ser His Gly Gly Val Leu Ala Lys Ala 290 295 300		
Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser 305 310 315 320		
Asp Trp Leu Tyr Pro Thr Ala Glu Asn Arg His Leu Val Arg Ala Leu 325 330 335		
Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys 340 345 350		
Gly His Asp Ala Phe Leu Leu Asp Glu Pro Val Met Asp Ala Ala Leu 355 360 365		
Glu Gly Phe Leu Ala Ser Ala Glu Arg Asp Arg Gly Leu Val 370 375 380		

<210> 11

<211> 1140

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS
 <222> (1)..(1137)
 <223> RNG00132

<400> 11

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ttt gaa atg ccg ctg gtt ttg gaa aac ggt aaa act ttg ccg cgt ttc	96
Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe	
20 25 30	
gat ctg atg att gaa acc tac ggc gag ctg aat gct gaa aaa aac aat	144
Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn	
35 40 45	
gcg gtt tta atc tgc cac gcg ctg tcg ggc aac cat cac gtt gcg ggc	192
Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly	
50 55 60	
agg cat tcg gcg gag gat aaa tat acg ggc tgg tgg gac aat atg gtc	240
Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val	
65 70 75 80	
ggg ccc gga aaa ccg att gat acg gaa cgt ttt ttc gtg gtc ggg ttg	288
Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu	
85 90 95	
aac aat ctg ggc ggc tgc gac ggc agc agc ggg cct ttg tcg atc aat	336
Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn	
100 105 110	
cct gaa acg ggc agg gaa tac ggc gcg gat ttt ccg atg gtt acg gtg	384
Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Met Val Thr Val	
115 120 125	
aag gac tgg gta aaa tca caa gcc gcg ctt gcc gat tat ctc ggc atc	432
Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Ala Asp Tyr Leu Gly Ile	
130 135 140	
gaa caa tgg gcg gcg gtt gtc ggc ggc agc ttg ggc ggc atg cag gct	480
Glu Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala	
145 150 155 160	
ttg cag tgg gcg att tcc tat ccc gaa cgt gtg cgc cac gcc ttg gtg	528
Leu Gln Trp Ala Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val	
165 170 175	
att gcg tct gcg ccg aaa ctg tcc gcg caa aat atc gcg ttt aat gat	576
Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Asp	
180 185 190	
gta gca cgt cag gcg att ttg acc gac ccc gat ttc aat gaa gga cat	624
Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His	
195 200 205	
tac cgc agc cac aac acc gtt ccc gcg cgc ggt ttg cgg att gcc cgt	672
Tyr Arg Ser His Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg	
210 215 220	

atg atg gga cac att acg tat ctt gcc gaa gac ggt ttg ggc aaa aaa 720
 Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys
 225 230 235 240

 ttc gga cgc gat ttg cgt tcc aac ggc tat caa tac ggc tat agc gtt 768
 Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Ser Val
 245 250 255

 gaa ttt gaa gta gaa tcc tat ctc cgc tat caa ggc gac aaa ttc gtc 816
 Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val
 260 265 270

 ggg cgg ttt gat gct aat aca tat ttg ctg atg acc aaa gct ttg gac 864
 Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp
 275 280 285

 tat ttc gat ccg gcg gcg gat ttc ggc aac agc ctg acc cgc gcc gtg 912
 Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val
 290 295 300

 cag gat gtg cag gca aaa ttc ttt gtc gcc agc ttc agc acc gac tgg 960
 Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp
 305 310 315 320

 cgt ttc gcg ccc gaa cgt tcg cac gaa ctg gtc aag gca ctg att gcc 1008
 Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala
 325 330 335

 gcc caa aaa tcc gtg cag tat atc gaa gtc aag tcc gca cac ggg cac 1056
 Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His
 340 345 350

 gat gcc ttt tta atg gaa gac gaa gcc tat atg cgc gcc gta acg gct 1104
 Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Thr Ala
 355 360 365

 tat atg aac aat gtt gac aag gat tgc cga tta tga 1140
 Tyr Met Asn Asn Val Asp Lys Asp Cys Arg Leu
 370 375

<210> 12

<211> 379

<212> PRT

<213> Neisseria gonorrhoeae

<400> 12

Met Ser Gln Asn Thr Ser Val Gly Ile Val Thr Pro Gln Lys Ile Pro
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Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe
20 25 30

Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
35 40 45

Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
50 55 60

Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
 65 70 75 80
 Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95
 Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100 105 110
 Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Met Val Thr Val
 115 120 125
 Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Ala Asp Tyr Leu Gly Ile
 130 135 140
 Glu Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala
 145 150 155 160
 Leu Gln Trp Ala Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
 165 170 175
 Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Asp
 180 185 190
 Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His
 195 200 205
 Tyr Arg Ser His Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg
 210 215 220
 Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys
 225 230 235 240
 Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Ser Val
 245 250 255
 Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val
 260 265 270
 Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp
 275 280 285
 Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val
 290 295 300
 Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp
 305 310 315 320
 Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala
 325 330 335
 Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His
 340 345 350
 Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Thr Ala
 355 360 365
 Tyr Met Asn Asn Val Asp Lys Asp Cys Arg Leu
 370 375

<210> 13
 <211> 1140
 <212> DNA
 <213> Neisseria meningitidis ser. A

<220>
 <221> CDS
 <222> (1)..(1137)
 <223> RNM00815

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 1 5 10 15
 ttt gaa atg ccg ctg gtt ttg gaa aac ggt aaa act ttg ccg cgt ttc 96
 Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe
 20 25 30
 gat ctg atg att gaa acc tac ggc gag ctg aat gcc gaa aaa aat aat 144
 Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
 35 40 45
 gcg gtt tta atc tgt cat gcg ctg tca ggc aac cat cat gtt gcg ggc 192
 Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
 50 55 60
 agg cat tcg gcg gag gat aaa tat acg ggc tgg tgg gac aat atg gta 240
 Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
 65 70 75 80
 gga ccc ggc aaa ccg att gat aca gaa cgt ttt ttc gtg gtc ggt ttg 288
 Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95
 aac aat ctg ggc ggc tgc gac ggc agc agc gga cct ttg tcg atc aat 336
 Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100 105 110
 cct gaa acg ggc agg gaa tac ggc gcg gat ttt ccg gtg gtt acg gtg 384
 Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Val Val Thr Val
 115 120 125
 aag gac tgg gta aaa tcc caa gcc gcg ctt acc gat tat ctc ggc atc 432
 Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Thr Asp Tyr Leu Gly Ile
 130 135 140
 ggg caa tgg gcg gcg gtt gtc ggc ggc agc ttg ggc ggt atg cag gct 480
 Gly Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala
 145 150 155 160
 ttg cag tgg acg att tcc tat ccc gag cgc gtg cgc cat gcc tta gtg 528
 Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
 165 170 175
 att gcg tcc gcg ccg aaa ctg tcc acg caa aat atc gcg ttt aat gat 576
 Ile Ala Ser Ala Pro Lys Leu Ser Thr Gln Asn Ile Ala Phe Asn Asp
 180 185 190

gta gca cgt cag gcg att ttg acc gat ccc gat ttc aac gaa gga cat	624
Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His	
195 200 205	
tac cgc agc cgc aac acc gtt ccc gct cgg ggc ttg cgg att gcc cgc	672
Tyr Arg Ser Arg Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg	
210 215 220	
atg atg ggg cac atc acc tat ctt gcc gaa gac ggt ttg ggc aaa aaa	720
Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys	
225 230 235 240	
ttc gga cgc gat ttg cgt tcc aac ggc tat caa tac ggc tat ggc gtt	768
Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Gly Val	
245 250 255	
gaa ttt gaa gta gaa tcc tat ctg cgc tat caa ggc gat aaa ttc gtc	816
Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val	
260 265 270	
ggg cgg ttt gat gcc aac acc tat ttg ctg atg acc aag gct ttg gac	864
Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp	
275 280 285	
tat ttc gat cgc gcg gcg gat ttc ggc aac agc ctg acc cgc gcc gtg	912
Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val	
290 295 300	
cag gat gtt cag gca aaa ttc ttt gtc gcc agc ttc agc acc gat tgg	960
Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp	
305 310 315 320	
cgt ttc gcg ccc gaa cgt tcg cac gaa ctg gtc aag gcc ctg att gcc	1008
Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala	
325 330 335	
gcc caa aaa tcc gtg cag tat atc gaa gtc aaa tcc gca cac ggg cac	1056
Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His	
340 345 350	
gat gcc ttt tta atg gaa gac gaa gcc tat atg cgt gcg gtc gcc gcc	1104
Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Ala Ala	
355 360 365	
tat atg aac aac gtt tat aag gaa tgt cag caa tga	1140
Tyr Met Asn Asn Val Tyr Lys Glu Cys Gln Gln	
370 375	

<210> 14

<211> 379

<212> PRT

<213> Neisseria meningitidis ser. A

<400> 14

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20

25

30

Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
 35 40 45
 Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
 50 55 60
 Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
 65 70 75 80
 Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95
 Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100 105 110
 Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Val Val Thr Val
 115 120 125
 Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Thr Asp Tyr Leu Gly Ile
 130 135 140
 Gly Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala
 145 150 155 160
 Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
 165 170 175
 Ile Ala Ser Ala Pro Lys Leu Ser Thr Gln Asn Ile Ala Phe Asn Asp
 180 185 190
 Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His
 195 200 205
 Tyr Arg Ser Arg Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg
 210 215 220
 Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys
 225 230 235 240
 Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Gly Val
 245 250 255
 Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val
 260 265 270
 Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp
 275 280 285
 Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val
 290 295 300
 Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp
 305 310 315 320
 Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala
 325 330 335
 Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His

340

345

350

Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Ala Ala
 355 360 365

Tyr Met Asn Asn Val Tyr Lys Glu Cys Gln Gln
 370 375

<210> 15

<211> 1140

<212> DNA

<213> Pseudomonas fluorescens

<220>

<221> CDS

<222> (1)..(1137)

<223> RPU01633

<400> 15

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acg gcg cac ttc agc gaa ccg ctg gcc ctg gcc tgc ggc cgt tcg ctg 96
 Thr Ala His Phe Ser Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu
 20 25 30

gcc gat tat gac ctg atc tac gaa acc tac ggc acg ctg aac gcg caa 144
 Ala Asp Tyr Asp Leu Ile Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Gln
 35 40 45

gcg agc aac gcc gtg ctg atc tgc cac gcc ttg tcc ggc cac cac cat 192
 Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60

gct gcg ggt tat cac agc gtc gac gac cgc aag ccc ggt tgg tgg gac 240
 Ala Ala Gly Tyr His Ser Val Asp Asp Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80

agc tgc atc ggc ccc ggc aaa ccg atc gac acc aac aag ttc ttc gtg 288
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Lys Phe Phe Val
 85 90 95

gtc agc ctg aac aac ctc ggc ggt tgc aat ggt tct acc ggc ccg agc 336
 Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser
 100 105 110

agc ctc aat ccg gaa acc ggc aag ccg ttc ggc gcc gac ttc ccg gtg 384
 Ser Leu Asn Pro Glu Thr Gly Lys Pro Phe Gly Ala Asp Phe Pro Val
 115 120 125

ctg acc gtg gaa gac tgg gtg cac agc cag gca cgc ctg gcc gac ctg 432
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Leu
 130 135 140

ctc ggc atc ggc cag tgg gcg gcg gtg atc ggc ggc agc ctg ggc ggc 480
 Leu Gly Ile Gly Gln Trp Ala Ala Val Ile Gly Gly Ser Leu Gly Gly
 145 150 155 160

atg cag gcg ctg caa tgg acc atc acc tat ccg gat cgc gtt cgc cac	528
Met Gln Ala Leu Gln Trp Thr Ile Thr Tyr Pro Asp Arg Val Arg His	
165 170 175	
tgc ctg gcc atc gcc tcg gcc ccc aag ctg tcg gcg cag aac atc gcc	576
Cys Leu Ala Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala	
180 185 190	
ttc aac gaa gtg gcg cgc cag gcg atc ctc act gac ccg gaa ttc cac	624
Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Phe His	
195 200 205	
ggc ggc tcg ttc cag gaa cac ggc gtg atc ccc aag cgc ggc ctg atg	672
Gly Gly Ser Phe Gln Glu His Gly Val Ile Pro Lys Arg Gly Leu Met	
210 215 220	
ctg gcg cgg atg gtg ggg cac atc acc tac ctg tcc gac gac tcc atg	720
Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met	
225 230 235 240	
ggg gag aaa ttc ggc cgt ggc ctg aag agc gaa aag ctc aac tac gac	768
Gly Glu Lys Phe Gly Arg Gly Leu Lys Ser Glu Lys Leu Asn Tyr Asp	
245 250 255	
ttc cac agc gtc gag ttc cag gtc gaa agc tac ctg cgc tat cag ggc	816
Phe His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly	
260 265 270	
gaa gag ttc tcc ggg cgc ttc gat gcc aac acc tat ctg ttg atg acc	864
Glu Glu Phe Ser Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr	
275 280 285	
aag gcg ctg gac tac ttc gat ccg gcg gcg aac ttc aac gat aac ctg	912
Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Asn Phe Asn Asp Asn Leu	
290 295 300	
gcg aaa acc ttc gaa ggt gca aaa gcc aag ttc tgc gtg atg tcg ttc	960
Ala Lys Thr Phe Glu Gly Ala Lys Ala Lys Phe Cys Val Met Ser Phe	
305 310 315 320	
acc acc gac tgg cgc ttc tcc ccg gcc cgc tcg cga gaa ctg gtg gat	1008
Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Leu Val Asp	
325 330 335	
gcg ctg atg gcg gcg cgc aaa gac gtc agc tac ctg gaa atc gac gcg	1056
Ala Leu Met Ala Ala Arg Lys Asp Val Ser Tyr Leu Glu Ile Asp Ala	
340 345 350	
ccc cag ggc cac gac gcc ttc ctg att ccg atc ccg cgc tac ttg cag	1104
Pro Gln Gly His Asp Ala Phe Leu Ile Pro Ile Pro Arg Tyr Leu Gln	
355 360 365	
gcg ttc ggc aat tac atg aac cgc att acg ttg tga	1140
Ala Phe Gly Asn Tyr Met Asn Arg Ile Thr Leu	
370 375	

<210> 16
 <211> 379
 <212> PRT

<213> *Pseudomonas fluorescens*

<400> 16

Met Pro Ala Ala Phe Pro Pro Asp Ser Val Gly Leu Val Thr Pro Gln
 1 5 10 15
 Thr Ala His Phe Ser Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu
 20 25 30
 Ala Asp Tyr Asp Leu Ile Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Gln
 35 40 45
 Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60
 Ala Ala Gly Tyr His Ser Val Asp Asp Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Lys Phe Phe Val
 85 90 95
 Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser
 100 105 110
 Ser Leu Asn Pro Glu Thr Gly Lys Pro Phe Gly Ala Asp Phe Pro Val
 115 120 125
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Leu
 130 135 140
 Leu Gly Ile Gly Gln Trp Ala Ala Val Ile Gly Gly Ser Leu Gly Gly
 145 150 155 160
 Met Gln Ala Leu Gln Trp Thr Ile Thr Tyr Pro Asp Arg Val Arg His
 165 170 175
 Cys Leu Ala Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Phe His
 195 200 205
 Gly Gly Ser Phe Gln Glu His Gly Val Ile Pro Lys Arg Gly Leu Met
 210 215 220
 Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met
 225 230 235 240
 Gly Glu Lys Phe Gly Arg Gly Leu Lys Ser Glu Lys Leu Asn Tyr Asp
 245 250 255
 Phe His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly
 260 265 270
 Glu Glu Phe Ser Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr
 275 280 285
 Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Asn Phe Asn Asp Asn Leu
 290 295 300

Ala Lys Thr Phe Glu Gly Ala Lys Ala Lys Phe Cys Val Met Ser Phe
305 310 315 320

Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Leu Val Asp
325 330 335

Ala Leu Met Ala Ala Arg Lys Asp Val Ser Tyr Leu Glu Ile Asp Ala
340 345 350

Pro Gln Gly His Asp Ala Phe Leu Ile Pro Ile Pro Arg Tyr Leu Gln
355 360 365

Ala Phe Gly Asn Tyr Met Asn Arg Ile Thr Leu
370 375

<210> 17

<211> 1140

<212> DNA

<213> Pseudomonas aeruginosa

<220>

<221> CDS

<222> (1)..(1137)

<223> RPA04460

<400> 17

atg ccc aca gtc ttc ccc gac gac tcc gtc ggt ctg gtc tcc ccc cag 48
Met Pro Thr Val Phe Pro Asp Asp Ser Val Gly Leu Val Ser Pro Gln
1 5 10 15

acg ctg cac ttc aac gaa ccg ctc gag ctg acc agc ggc aag tcc ctg 96
Thr Leu His Phe Asn Glu Pro Leu Glu Leu Thr Ser Gly Lys Ser Leu
20 25 30

gcc gag tac gac ctg gtg atc gaa acc tac ggc gag ctg aat gcc acg 144
Ala Glu Tyr Asp Leu Val Ile Glu Thr Tyr Gly Glu Leu Asn Ala Thr
35 40 45

cag agc aac gcg gtg ctg atc tgc cac gcc ctc tcc ggc cac cac cac 192
Gln Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
50 55 60

gcc gcc ggc tac cac agc gtc gac gag cgc aag ccg ggc tgg tgg gac 240
Ala Ala Gly Tyr His Ser Val Asp Glu Arg Lys Pro Gly Trp Trp Asp
65 70 75 80

agc tgc atc ggt ccg ggc aag ccg atc gac acc cgc aag ttc ttc gtc 288
Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Arg Lys Phe Phe Val
85 90 95

gtc gcc ctc aac aac ctc ggc ggt tgc aac gga tcc agc ggc ccc gcc 336
Val Ala Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Ser Gly Pro Ala
100 105 110

agc atc aat ccg gcg acc ggc aag gtc tac ggc gcg gac ttc ccg atg 384
Ser Ile Asn Pro Ala Thr Gly Lys Val Tyr Gly Ala Asp Phe Pro Met
115 120 125

gtt acg gtg gaa gac tgg gtg cat agc cag gcg cgc ctg gca gac cgc 432

Val Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg	
130 135 140	
ctc ggc atc cgc cag tgg gcc gcg gtg gtc ggc ggc agc ctc ggc ggc	480
Leu Gly Ile Arg Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly	
145 150 155 160	
atg cag gcg ctg caa tgg acc atc agc tat ccc gag cgc gtc cgt cac	528
Met Gln Ala Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His	
165 170 175	
tgc ctg tgc atc gcc agc gcg ccg aag ctg tcg gcg cag aac atc gcc	576
Cys Leu Cys Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala	
180 185 190	
ttc aac gaa gtc gcc cgg cag gcg att ctt tcc gac cct gag ttc ctc	624
Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Ser Asp Pro Glu Phe Leu	
195 200 205	
ggc ggc tac ttc cag gag cag gcc gtg att ccc aag cgc ggc ctc aag	672
Gly Gly Tyr Phe Gln Glu Gln Gly Val Ile Pro Lys Arg Gly Leu Lys	
210 215 220	
ctg gcg cgg atg gtc gcc cat atc acc tac ctg tcc gac gac gcc atg	720
Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ala Met	
225 230 235 240	
ggc gcc aag ttc gcc cgt gta ctg aag acc gag aag ctc aac tac gac	768
Gly Ala Lys Phe Gly Arg Val Leu Lys Thr Glu Lys Leu Asn Tyr Asp	
245 250 255	
ctg cac agc gtc gag ttc cag gtc gag agt tac ctg cgc tac cag ggc	816
Leu His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly	
260 265 270	
gag gag ttc tcc acc cgc ttc gac gcc aat acc tac ctg ctg atg acc	864
Glu Glu Phe Ser Thr Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr	
275 280 285	
aag gcg ctg gac tac ttc gac ccc gcc gcc gcc cac ggc gac gac ctg	912
Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Ala His Gly Asp Asp Leu	
290 295 300	
gtg cgc acc ctg gag gcc gtc gag gcg gac ttc tgc ctg atg tcc ttc	960
Val Arg Thr Leu Glu Gly Val Glu Ala Asp Phe Cys Leu Met Ser Phe	
305 310 315 320	
acc acc gac tgg cgt ttc tcg ccg gcc cgc tcg cgg gaa atc gtc gac	1008
Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Ile Val Asp	
325 330 335	
gcc ctg atc gcg gcg aaa aag aac gtc agc tac ctg gag atc gac gcc	1056
Ala Leu Ile Ala Ala Lys Lys Asn Val Ser Tyr Leu Glu Ile Asp Ala	
340 345 350	
ccg caa ggc cac gac gcc ttc ctc atg ccg atc ccc cgg tac ctg caa	1104
Pro Gln Gly His Asp Ala Phe Leu Met Pro Ile Pro Arg Tyr Leu Gln	
355 360 365	
gcc ttc agc ggt tac atg aac cgc atc agc gtg tga	1140

Ala Phe Ser Gly Tyr Met Asn Arg Ile Ser Val
370 375

<210> 18

<211> 379

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 18

Met Pro Thr Val Phe Pro Asp Asp Ser Val Gly Leu Val Ser Pro Gln
1 5 10 15

Thr Leu His Phe Asn Glu Pro Leu Glu Leu Thr Ser Gly Lys Ser Leu
20 25 30

Ala Glu Tyr Asp Leu Val Ile Glu Thr Tyr Gly Glu Leu Asn Ala Thr
35 40 45

Gln Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
50 55 60

Ala Ala Gly Tyr His Ser Val Asp Glu Arg Lys Pro Gly Trp Trp Asp
65 70 75 80

Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Arg Lys Phe Phe Val
85 90 95

Val Ala Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Ser Gly Pro Ala
100 105 110

Ser Ile Asn Pro Ala Thr Gly Lys Val Tyr Gly Ala Asp Phe Pro Met
115 120 125

Val Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
130 135 140

Leu Gly Ile Arg Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly
145 150 155 160

Met Gln Ala Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His
165 170 175

Cys Leu Cys Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
180 185 190

Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Ser Asp Pro Glu Phe Leu
195 200 205

Gly Gly Tyr Phe Gln Glu Gln Gly Val Ile Pro Lys Arg Gly Leu Lys
210 215 220

Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ala Met
225 230 235 240

Gly Ala Lys Phe Gly Arg Val Leu Lys Thr Glu Lys Leu Asn Tyr Asp
245 250 255

Leu His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly
260 265 270

Glu Glu Phe Ser Thr Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr
 275 280 285

Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Ala His Gly Asp Asp Leu
 290 295 300

Val Arg Thr Leu Glu Gly Val Glu Ala Asp Phe Cys Leu Met Ser Phe
 305 310 315 320

Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Ile Val Asp
 325 330 335

Ala Leu Ile Ala Ala Lys Lys Asn Val Ser Tyr Leu Glu Ile Asp Ala
 340 345 350

Pro Gln Gly His Asp Ala Phe Leu Met Pro Ile Pro Arg Tyr Leu Gln
 355 360 365

Ala Phe Ser Gly Tyr Met Asn Arg Ile Ser Val
 370 375

<210> 19

<211> 1146

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (1)..(1143)

<223> RBU12675

<400> 19

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 Met Glu Ser Ile Gly Ile Val Ala Pro Gln Lys Met His Phe Thr Glu
 1 5 10 15

ccg ctg ccg ttg cag aac ggc agt tcg ctc gcc ggt tac gac ctg atg 96
 Pro Leu Pro Leu Gln Asn Gly Ser Ser Leu Ala Gly Tyr Asp Leu Met
 20 25 30

gtc gag acc tac ggc acg ctc aac gcc gcg cgt agc aac gcg gtg ctg 144
 Val Glu Thr Tyr Gly Thr Leu Asn Ala Ala Arg Ser Asn Ala Val Leu
 35 40 45

gtg tgc cac gcg ctc aac gcg tcg cac cac gtg gcg ggc gtg tat gcc 192
 Val Cys His Ala Leu Asn Ala Ser His His Val Ala Gly Val Tyr Ala
 50 55 60

gac aac ccc agg gac atc ggc tgg tgg gac aac atg gtc ggc ccg ggc 240
 Asp Asn Pro Arg Asp Ile Gly Trp Trp Asp Asn Met Val Gly Pro Gly
 65 70 75 80

aag ccg ctc gac act gac aag ttc ttc gtg atc ggc gtg aac aac ctc 288
 Lys Pro Leu Asp Thr Asp Lys Phe Phe Val Ile Gly Val Asn Asn Leu
 85 90 95

gga tcg tgc ttc ggc tcg act ggg ccg atg agc atc gat ccg tct acc 336
 Gly Ser Cys Phe Gly Ser Thr Gly Pro Met Ser Ile Asp Pro Ser Thr

100	105	110	
ggc aat ccg tac ggc gcg acg ttt ccc gtc gtg acg gtg gaa gac tgg			384
Gly Asn Pro Tyr Gly Ala Thr Phe Pro Val Val Thr Val Glu Asp Trp			
115	120	125	
gtc aac gcc cag gcg cgc gtc gcg gat caa ttc ggc atc acg cgc ttt			432
Val Asn Ala Gln Ala Arg Val Ala Asp Gln Phe Gly Ile Thr Arg Phe			
130	135	140	
gcg gcg gtg atg ggc ggc agc ctc ggc ggc atg cag gcg ctc gcg tgg			480
Ala Ala Val Met Gly Gly Ser Leu Gly Gly Met Gln Ala Leu Ala Trp			
145	150	155	160
agc atg atg tat ccg gag cgc gtc gct cac tgc atc gtg gtc gcg tcc			528
Ser Met Met Tyr Pro Glu Arg Val Ala His Cys Ile Val Val Ala Ser			
165	170	175	
aca ccc aag ctg tcg gcg cag aac atc gcg ttc aac gag gtt gcg cgc			576
Thr Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Glu Val Ala Arg			
180	185	190	
tcg gcg atc ctg tcg gac ccg gac ttc cac ggc ggc aac tac tac gcg			624
Ser Ala Ile Leu Ser Asp Pro Asp Phe His Gly Gly Asn Tyr Tyr Ala			
195	200	205	
cac aac gtt aag ccg aag cgc ggc ctg cgc gtc gcg cgc atg atc ggc			672
His Asn Val Lys Pro Lys Arg Gly Leu Arg Val Ala Arg Met Ile Gly			
210	215	220	
cac atc acg tat ctg tcg gac gac gac atg gcc gag aaa ttc ggc cgc			720
His Ile Thr Tyr Leu Ser Asp Asp Asp Met Ala Glu Lys Phe Gly Arg			
225	230	235	240
tcg ctg cgg cgc gcg gaa ggc gcg ctg gac gcg tac aac ttc aac ttc			768
Ser Leu Arg Arg Ala Glu Gly Ala Leu Asp Ala Tyr Asn Phe Asn Phe			
245	250	255	
gac gtg gag ttc gag gtg gag tcg tac ctg cgc tac cag ggc gac aag			816
Asp Val Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys			
260	265	270	
ttc gcc gac tac ttc gac gcg aat acg tat ctg ctg atc acc cgc gcg			864
Phe Ala Asp Tyr Phe Asp Ala Asn Thr Tyr Leu Leu Ile Thr Arg Ala			
275	280	285	
ctc gac tac ttc gat ccg gcc aag gcc ttc gcc ggc gac ctg acg gcc			912
Leu Asp Tyr Phe Asp Pro Ala Lys Ala Phe Ala Gly Asp Leu Thr Ala			
290	295	300	
gcg gtc gcg cac acc acg gcg aaa tat ctg atc gcc agc ttc acg acc			960
Ala Val Ala His Thr Thr Ala Lys Tyr Leu Ile Ala Ser Phe Thr Thr			
305	310	315	320
gac tgg cgc ttc gcg ccg gcc cgc tcg cgt gaa ctg gtg aag gcg ctg			1008
Asp Trp Arg Phe Ala Pro Ala Arg Ser Arg Glu Leu Val Lys Ala Leu			
325	330	335	
ctc gat cac aag cgc acg gtc acc tac gcg gaa atc gac gcg ccg cac			1056
Leu Asp His Lys Arg Thr Val Thr Tyr Ala Glu Ile Asp Ala Pro His			

340

345

350

ggc cac gac gcc ttc ctg ctc gac gac gcg cgc tat cac aac ctg atg 1104
 Gly His Asp Ala Phe Leu Leu Asp Asp Ala Arg Tyr His Asn Leu Met
 355 360 365

cgc gct tac tac gaa cgt att gcg aac gag gtg aac gca tga 1146
 Arg Ala Tyr Tyr Glu Arg Ile Ala Asn Glu Val Asn Ala
 370 375 380

<210> 20

<211> 381

<212> PRT

<213> Burkholderia cepacia

<400> 20

Met Glu Ser Ile Gly Ile Val Ala Pro Gln Lys Met His Phe Thr Glu
 1 5 10 15

Pro Leu Pro Leu Gln Asn Gly Ser Ser Leu Ala Gly Tyr Asp Leu Met
 20 25 30

Val Glu Thr Tyr Gly Thr Leu Asn Ala Ala Arg Ser Asn Ala Val Leu
 35 40 45

Val Cys His Ala Leu Asn Ala Ser His His Val Ala Gly Val Tyr Ala
 50 55 60

Asp Asn Pro Arg Asp Ile Gly Trp Trp Asp Asn Met Val Gly Pro Gly
 65 70 75 80

Lys Pro Leu Asp Thr Asp Lys Phe Phe Val Ile Gly Val Asn Asn Leu
 85 90 95

Gly Ser Cys Phe Gly Ser Thr Gly Pro Met Ser Ile Asp Pro Ser Thr
 100 105 110

Gly Asn Pro Tyr Gly Ala Thr Phe Pro Val Val Thr Val Glu Asp Trp
 115 120 125

Val Asn Ala Gln Ala Arg Val Ala Asp Gln Phe Gly Ile Thr Arg Phe
 130 135 140

Ala Ala Val Met Gly Gly Ser Leu Gly Gly Met Gln Ala Leu Ala Trp
 145 150 155 160

Ser Met Met Tyr Pro Glu Arg Val Ala His Cys Ile Val Val Ala Ser
 165 170 175

Thr Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Glu Val Ala Arg
 180 185 190

Ser Ala Ile Leu Ser Asp Pro Asp Phe His Gly Gly Asn Tyr Tyr Ala
 195 200 205

His Asn Val Lys Pro Lys Arg Gly Leu Arg Val Ala Arg Met Ile Gly
 210 215 220

His Ile Thr Tyr Leu Ser Asp Asp Asp Met Ala Glu Lys Phe Gly Arg

225	230	235	240
Ser Leu Arg Arg Ala Glu Gly Ala Leu Asp Ala Tyr Asn Phe Asn Phe	245	250	255
Asp Val Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys	260	265	270
Phe Ala Asp Tyr Phe Asp Ala Asn Thr Tyr Leu Leu Ile Thr Arg Ala	275	280	285
Leu Asp Tyr Phe Asp Pro Ala Lys Ala Phe Ala Gly Asp Leu Thr Ala	290	295	300
Ala Val Ala His Thr Thr Ala Lys Tyr Leu Ile Ala Ser Phe Thr Thr	305	310	315
Asp Trp Arg Phe Ala Pro Ala Arg Ser Arg Glu Leu Val Lys Ala Leu	325	330	335
Leu Asp His Lys Arg Thr Val Thr Tyr Ala Glu Ile Asp Ala Pro His	340	345	350
Gly His Asp Ala Phe Leu Leu Asp Asp Ala Arg Tyr His Asn Leu Met	355	360	365
Arg Ala Tyr Tyr Glu Arg Ile Ala Asn Glu Val Asn Ala	370	375	380

<210> 21
 <211> 1134
 <212> DNA
 <213> Nitrosomonas europaea

<220>
 <221> CDS
 <222> (1) .. (1131)
 <223> RNE02005

<400> 21	
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Met Ser Thr Gln Asp Ser Asp Ser Ile Gly Ile Val Ser Ala Arg Arg	
1 5 10 15	
gcc cat ttc gac acc ccg ctc agc ctg aaa agc gga gct gta ctg gac	96
Ala His Phe Asp Thr Pro Leu Ser Leu Lys Ser Gly Ala Val Leu Asp	
20 25 30	
agc tac gag ctc gtc tat gaa acc tat ggg gag ctg aat gca gac cga	144
Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Glu Leu Asn Ala Asp Arg	
35 40 45	
tcc aat gca gtg ctg atc tgc cat gct tta tcc ggc aac cac cat gtt	192
Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val	
50 55 60	
gcc ggt gtt tat gca gat aac ccc aag aat acc gga tgg tgg aac aac	240
Ala Gly Val Tyr Ala Asp Asn Pro Lys Asn Thr Gly Trp Trp Asn Asn	
65 70 75 80	

atg atc ggt ccg ggc aaa ccg gtc gat acc cga aaa ttc ttt gtc atc	288
Met Ile Gly Pro Gly Lys Pro Val Asp Thr Arg Lys Phe Phe Val Ile	
85 90 95	
ggg atc aat aat ctc ggg ggt tgc cat ggc tcc acc ggg ccc atc agc	336
Gly Ile Asn Asn Leu Gly Gly Cys His Gly Ser Thr Gly Pro Ile Ser	
100 105 110	
atc aac gac aag acc ggt aaa cgc ttc ggc ccg gat ttt ccg ctg gta	384
Ile Asn Asp Lys Thr Gly Lys Arg Phe Gly Pro Asp Phe Pro Leu Val	
115 120 125	
acg aca gct gac tgg gca aaa acc tat gtc cgt ttc gcc gat cag ttc	432
Thr Thr Ala Asp Trp Ala Lys Thr Tyr Val Arg Phe Ala Asp Gln Phe	
130 135 140	
agc atc gac tgt ttt gcc gcc gtc atc ggt ggc agt ctg ggc ggg atg	480
Ser Ile Asp Cys Phe Ala Ala Val Ile Gly Gly Ser Leu Gly Gly Met	
145 150 155 160	
tcg gcc atg caa ctg gcg ctc gat gca ccg gaa aga gtt cgt cat gcc	528
Ser Ala Met Gln Leu Ala Leu Asp Ala Pro Glu Arg Val Arg His Ala	
165 170 175	
ata gtg gtt gca gca tcg gcc agg ctg aca gca cag aac atc gct ttc	576
Ile Val Val Ala Ala Ser Ala Arg Leu Thr Ala Gln Asn Ile Ala Phe	
180 185 190	
aat gat gtc gcg cgt cag gcg att ctg acc gac cct gat ttt cac gac	624
Asn Asp Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe His Asp	
195 200 205	
ggc gac tat tat tcc cat ggc acc cac ccg cgc aga ggt tta cgc ctt	672
Gly Asp Tyr Tyr Ser His Gly Thr His Pro Arg Arg Gly Leu Arg Leu	
210 215 220	
gcc cgc atg ctt ggc cac atc acc tac ctg tcg gac gac tcc atg gcc	720
Ala Arg Met Leu Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met Ala	
225 230 235 240	
agc aaa ttc ggc cgt gag tta cgt aac ggc tcg ctt gct ttc aat tat	768
Ser Lys Phe Gly Arg Glu Leu Arg Asn Gly Ser Leu Ala Phe Asn Tyr	
245 250 255	
gat gtg gaa ttc cag atc gaa tcc tat ctg cac cat cag ggc gac aaa	816
Asp Val Glu Phe Gln Ile Glu Ser Tyr Leu His His Gln Gly Asp Lys	
260 265 270	
ttt gcc gac ctg ttc gac gca aac act tat ctg ctg atg acg aag gcg	864
Phe Ala Asp Leu Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala	
275 280 285	
ctc gat tat ttc gat ccg gcc cag gat tac gat ggc aac ctg agt gca	912
Leu Asp Tyr Phe Asp Pro Ala Gln Asp Tyr Asp Gly Asn Leu Ser Ala	
290 295 300	
gcc ttt gcc cgt gca caa gcg gat ttt ctg gta ctt tcc ttt act tcc	960
Ala Phe Ala Arg Ala Gln Ala Asp Phe Leu Val Leu Ser Phe Thr Ser	
305 310 315 320	

gac tgg cgt ttt tcc ccg gag cgt tcg cgc gat atc gtc aag gca ctg 1008
 Asp Trp Arg Phe Ser Pro Glu Arg Ser Arg Asp Ile Val Lys Ala Leu
 325 330 335

ctc gac aac aaa ctg aat gtc agt tat gcg gaa att ccc tcc tcg tac 1056
 Leu Asp Asn Lys Leu Asn Val Ser Tyr Ala Glu Ile Pro Ser Ser Tyr
 340 345 350

gga cat gat tcc ttt ctc atg cag gac gac tac tat cac cag ttg ata 1104
 Gly His Asp Ser Phe Leu Met Gln Asp Asp Tyr Tyr His Gln Leu Ile
 355 360 365

cgt gct tac atg aac aat atc gct ctc tag 1134
 Arg Ala Tyr Met Asn Asn Ile Ala Leu
 370 375

<210> 22

<211> 377

<212> PRT

<213> Nitrosomonas europaea

<400> 22

Met Ser Thr Gln Asp Ser Asp Ser Ile Gly Ile Val Ser Ala Arg Arg
 1 5 10 15

Ala His Phe Asp Thr Pro Leu Ser Leu Lys Ser Gly Ala Val Leu Asp
 20 25 30

Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Glu Leu Asn Ala Asp Arg
 35 40 45

Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val
 50 55 60

Ala Gly Val Tyr Ala Asp Asn Pro Lys Asn Thr Gly Trp Trp Asn Asn
 65 70 75 80

Met Ile Gly Pro Gly Lys Pro Val Asp Thr Arg Lys Phe Phe Val Ile
 85 90 95

Gly Ile Asn Asn Leu Gly Gly Cys His Gly Ser Thr Gly Pro Ile Ser
 100 105 110

Ile Asn Asp Lys Thr Gly Lys Arg Phe Gly Pro Asp Phe Pro Leu Val
 115 120 125

Thr Thr Ala Asp Trp Ala Lys Thr Tyr Val Arg Phe Ala Asp Gln Phe
 130 135 140

Ser Ile Asp Cys Phe Ala Ala Val Ile Gly Gly Ser Leu Gly Gly Met
 145 150 155 160

Ser Ala Met Gln Leu Ala Leu Asp Ala Pro Glu Arg Val Arg His Ala
 165 170 175

Ile Val Val Ala Ala Ser Ala Arg Leu Thr Ala Gln Asn Ile Ala Phe
 180 185 190

Asn Asp Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe His Asp
195 200 205

Gly Asp Tyr Tyr Ser His Gly Thr His Pro Arg Arg Gly Leu Arg Leu
210 215 220

Ala Arg Met Leu Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met Ala
225 230 235 240

Ser Lys Phe Gly Arg Glu Leu Arg Asn Gly Ser Leu Ala Phe Asn Tyr
245 250 255

Asp Val Glu Phe Gln Ile Glu Ser Tyr Leu His His Gln Gly Asp Lys
260 265 270

Phe Ala Asp Leu Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala
275 280 285

Leu Asp Tyr Phe Asp Pro Ala Gln Asp Tyr Asp Gly Asn Leu Ser Ala
290 295 300

Ala Phe Ala Arg Ala Gln Ala Asp Phe Leu Val Leu Ser Phe Thr Ser
305 310 315 320

Asp Trp Arg Phe Ser Pro Glu Arg Ser Arg Asp Ile Val Lys Ala Leu
325 330 335

Leu Asp Asn Lys Leu Asn Val Ser Tyr Ala Glu Ile Pro Ser Ser Tyr
340 345 350

Gly His Asp Ser Phe Leu Met Gln Asp Asp Tyr Tyr His Gln Leu Ile
355 360 365

Arg Ala Tyr Met Asn Asn Ile Ala Leu
370 375

<210> 23

<211> 1077

<212> DNA

<213> Haemophilus influenzae

<220>

<221> CDS

<222> (1)..(1074)

<223> RHI02681

<400> 23

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Met Ser Val Gln Asn Val Val Leu Phe Asp Thr Gln Pro Leu Thr Leu
1 5 10 15

atg ctt ggc ggc aaa ctt tcc cat att aat gtc gcg tat caa act tat 96
Met Leu Gly Gly Lys Leu Ser His Ile Asn Val Ala Tyr Gln Thr Tyr
20 25 30

ggc acg ctc aat gcc gaa aaa aat aat gcg gta tta att tgc cac gct 144
Gly Thr Leu Asn Ala Glu Lys Asn Asn Ala Val Leu Ile Cys His Ala
35 40 45

ttg act ggt gat gct gag cct tat ttc gat gat ggt cga gat ggc tgg	192
Leu Thr Gly Asp Ala Glu Pro Tyr Phe Asp Asp Gly Arg Asp Gly Trp	
50 55 60	
tggt cag aat ttt atg gga gca ggt tta gca ttg gat acg gat cgt tat	240
Trp Gln Asn Phe Met Gly Ala Gly Leu Ala Leu Asp Thr Asp Arg Tyr	
65 70 75 80	
ttt ttt att agc tcg aac gta tta ggt ggt tgc aag gga aca act ggg	288
Phe Phe Ile Ser Ser Asn Val Leu Gly Gly Cys Lys Gly Thr Thr Gly	
85 90 95	
cct tca tca att aat ccg caa acg ggt aaa cct tat ggc agc caa ttt	336
Pro Ser Ser Ile Asn Pro Gln Thr Gly Lys Pro Tyr Gly Ser Gln Phe	
100 105 110	
cct aat att gtt gtg caa gat att gtt aaa gta caa aaa gcc ttg ctt	384
Pro Asn Ile Val Val Gln Asp Ile Val Lys Val Gln Lys Ala Leu Leu	
115 120 125	
gat cat ctt ggt att agc cat tta aaa gcc att att ggt gga tct ttt	432
Asp His Leu Gly Ile Ser His Leu Lys Ala Ile Ile Gly Gly Ser Phe	
130 135 140	
ggc ggc atg caa gcg aat caa tgg gcg att gat tat cct gat ttt atg	480
Gly Gly Met Gln Ala Asn Gln Trp Ala Ile Asp Tyr Pro Asp Phe Met	
145 150 155 160	
gat aat atc gtg aat ctt tgc tca tcc att tat ttt agt gct gaa gcc	528
Asp Asn Ile Val Asn Leu Cys Ser Ser Ile Tyr Phe Ser Ala Glu Ala	
165 170 175	
ata ggt ttt aat cac gta atg cgt caa gcg gtc att aat gat ccc aat	576
Ile Gly Phe Asn His Val Met Arg Gln Ala Val Ile Asn Asp Pro Asn	
180 185 190	
ttt aac ggc ggc gat tat tat gag ggt aca ccg cca gat caa ggg tta	624
Phe Asn Gly Gly Asp Tyr Tyr Glu Gly Thr Pro Pro Asp Gln Gly Leu	
195 200 205	
tct att gca cgt atg cta ggt atg ctg act tac cgc acc gat tta caa	672
Ser Ile Ala Arg Met Leu Gly Met Leu Thr Tyr Arg Thr Asp Leu Gln	
210 215 220	
ctt gcg aaa gcc ttt ggg cgt gcc aca aaa tca gat ggc agc ttt tgg	720
Leu Ala Lys Ala Phe Gly Arg Ala Thr Lys Ser Asp Gly Ser Phe Trp	
225 230 235 240	
ggc gat tac ttt caa gtg gaa tcc tat ctt tct tac caa ggc aaa aaa	768
Gly Asp Tyr Phe Gln Val Glu Ser Tyr Leu Ser Tyr Gln Gly Lys Lys	
245 250 255	
ttc tta gaa cgt ttt gat gcc aat agt tat ttg cat ttg tta cgt gcg	816
Phe Leu Glu Arg Phe Asp Ala Asn Ser Tyr Leu His Leu Leu Arg Ala	
260 265 270	
ttg gat atg tat gat cca agt ttg ggg tat gac aat gtt aaa gag gca	864
Leu Asp Met Tyr Asp Pro Ser Leu Gly Tyr Asp Asn Val Lys Glu Ala	
275 280 285	

tta tca cgt att aaa gca cgc tat acg ttg gtt tct gtg aca acg gat 912
 Leu Ser Arg Ile Lys Ala Arg Tyr Thr Leu Val Ser Val Thr Thr Asp
 290 295 300

caa ctt ttt aaa ccc att gat ctt tat aaa agt aaa cag ctt tta gag 960
 Gln Leu Phe Lys Pro Ile Asp Leu Tyr Lys Ser Lys Gln Leu Leu Glu
 305 310 315 320

caa agt gga gtc gat cta cat ttt tat gaa ttc cca tca gat tac gga 1008
 Gln Ser Gly Val Asp Leu His Phe Tyr Glu Phe Pro Ser Asp Tyr Gly
 325 330 335

cac gat gcg ttt tta gtg gat tat gat cag ttt gaa aaa cga att cga 1056
 His Asp Ala Phe Leu Val Asp Tyr Asp Gln Phe Glu Lys Arg Ile Arg
 340 345 350

gat ggt ttg gca ggt aat taa 1077
 Asp Gly Leu Ala Gly Asn
 355

<210> 24

<211> 358

<212> PRT

<213> Haemophilus influenzae

<400> 24

Met Ser Val Gln Asn Val Val Leu Phe Asp Thr Gln Pro Leu Thr Leu
 1 5 10 15

Met Leu Gly Gly Lys Leu Ser His Ile Asn Val Ala Tyr Gln Thr Tyr
 20 25 30

Gly Thr Leu Asn Ala Glu Lys Asn Asn Ala Val Leu Ile Cys His Ala
 35 40 45

Leu Thr Gly Asp Ala Glu Pro Tyr Phe Asp Asp Gly Arg Asp Gly Trp
 50 55 60

Trp Gln Asn Phe Met Gly Ala Gly Leu Ala Leu Asp Thr Asp Arg Tyr
 65 70 75 80

Phe Phe Ile Ser Ser Asn Val Leu Gly Gly Cys Lys Gly Thr Thr Gly
 85 90 95

Pro Ser Ser Ile Asn Pro Gln Thr Gly Lys Pro Tyr Gly Ser Gln Phe
 100 105 110

Pro Asn Ile Val Val Gln Asp Ile Val Lys Val Gln Lys Ala Leu Leu
 115 120 125

Asp His Leu Gly Ile Ser His Leu Lys Ala Ile Ile Gly Gly Ser Phe
 130 135 140

Gly Gly Met Gln Ala Asn Gln Trp Ala Ile Asp Tyr Pro Asp Phe Met
 145 150 155 160

Asp Asn Ile Val Asn Leu Cys Ser Ser Ile Tyr Phe Ser Ala Glu Ala
 165 170 175

Ile Gly Phe Asn His Val Met Arg Gln Ala Val Ile Asn Asp Pro Asn
 180 185 190
 Phe Asn Gly Gly Asp Tyr Tyr Glu Gly Thr Pro Pro Asp Gln Gly Leu
 195 200 205
 Ser Ile Ala Arg Met Leu Gly Met Leu Thr Tyr Arg Thr Asp Leu Gln
 210 215 220
 Leu Ala Lys Ala Phe Gly Arg Ala Thr Lys Ser Asp Gly Ser Phe Trp
 225 230 235 240
 Gly Asp Tyr Phe Gln Val Glu Ser Tyr Leu Ser Tyr Gln Gly Lys Lys
 245 250 255
 Phe Leu Glu Arg Phe Asp Ala Asn Ser Tyr Leu His Leu Leu Arg Ala
 260 265 270
 Leu Asp Met Tyr Asp Pro Ser Leu Gly Tyr Asp Asn Val Lys Glu Ala
 275 280 285
 Leu Ser Arg Ile Lys Ala Arg Tyr Thr Leu Val Ser Val Thr Thr Asp
 290 295 300
 Gln Leu Phe Lys Pro Ile Asp Leu Tyr Lys Ser Lys Gln Leu Leu Glu
 305 310 315 320
 Gln Ser Gly Val Asp Leu His Phe Tyr Glu Phe Pro Ser Asp Tyr Gly
 325 330 335
 His Asp Ala Phe Leu Val Asp Tyr Asp Gln Phe Glu Lys Arg Ile Arg
 340 345 350
 Asp Gly Leu Ala Gly Asn
 355

<210> 25

<211> 1296

<212> DNA

<213> Halobacterium sp

<220>

<221> CDS

<222> (1) .. (1293)

<223> ETX_HALN1

<400> 25

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cgc gtc gac ccg gcc acg ggc gct cgc gcg ccg cca ctc tac cag acc	96
Arg Val Asp Pro Ala Thr Gly Ala Arg Ala Pro Pro Leu Tyr Gln Thr	
20 25 30	
acg tcg tac gcc ttc gag gac agc gcc gat gcc gcc ggc cag ttc gcc	144
Thr Ser Tyr Ala Phe Glu Asp Ser Ala Asp Ala Ala Gly Gln Phe Ala	
35 40 45	

ctt gag cgg gac ggc tac atc tac tcg cgg ctg atg aac ccc acc gtg	192
Leu Glu Arg Asp Gly Tyr Ile Tyr Ser Arg Leu Met Asn Pro Thr Val	
50 55 60	
 gag acc ctc cag gac cgc ctc gcc gcc ctc gaa ggc ggc gtc ggc gcg	240
Glu Thr Leu Gln Asp Arg Leu Ala Ala Leu Glu Gly Gly Val Gly Ala	
65 70 75 80	
 gtc gcc acc gcg tcc gga atg gcc gcc ctg gac ctc gcg acg ttc ctg	288
Val Ala Thr Ala Ser Gly Met Ala Ala Leu Asp Leu Ala Thr Phe Leu	
85 90 95	
 ctg gca cgc gcc ggc gac tcc gtc gtc gcc gcc agc gac ctc tac ggc	336
Leu Ala Arg Ala Gly Asp Ser Val Val Ala Ala Ser Asp Leu Tyr Gly	
100 105 110	
 ggc acc gtg acg tac ctc acg cac agc gcc cag cgc cgc ggc gtc gac	384
Gly Thr Val Thr Tyr Leu Thr His Ser Ala Gln Arg Gly Val Asp	
115 120 125	
 acg acg ttc gtg gac gtc ctc gac tac gac gcc tac gcc gac gcc atc	432
Thr Thr Phe Val Asp Val Leu Asp Tyr Asp Ala Tyr Ala Asp Ala Ile	
130 135 140	
 gac gcc gac acc gcc tac gtg ctc gtc gaa acc gtc ggc aac ccc agc	480
Asp Ala Asp Thr Ala Tyr Val Leu Val Glu Thr Val Gly Asn Pro Ser	
145 150 155 160	
 ctg atc acg ccc gac ctc gaa cgc atc gcc gac atc gcc cac gac aac	528
Leu Ile Thr Pro Asp Leu Glu Arg Ile Ala Asp Ile Ala His Asp Asn	
165 170 175	
 ggc gtt ccc ctg ctg gtg gac aac acg ttc gcg acc ccc gcg ctg gca	576
Gly Val Pro Leu Leu Val Asp Asn Thr Phe Ala Thr Pro Ala Leu Ala	
180 185 190	
 acc ccg atc gac cac ggt gcc gac atc gtc tgg cac tcc acc acc aaa	624
Thr Pro Ile Asp His Gly Ala Asp Ile Val Trp His Ser Thr Thr Lys	
195 200 205	
 tgg atc cac ggt gcc ggc acc acc gtc ggc ggc gcg ctc gtc gac gcc	672
Trp Ile His Gly Ala Gly Thr Thr Val Gly Gly Ala Leu Val Asp Ala	
210 215 220	
 ggc agc ttc gac tgg gac gcc cac gcc gcc gac tac ccc gag atc gcc	720
Gly Ser Phe Asp Trp Asp Ala His Ala Ala Asp Tyr Pro Glu Ile Ala	
225 230 235 240	
 cag gaa aac ccc gcc tac cac ggc gtg acc ttc acc gat cgc ttc ggg	768
Gln Glu Asn Pro Ala Tyr His Gly Val Thr Phe Thr Asp Arg Phe Gly	
245 250 255	
 gac gcc gcg ttc acg tac gcc gca atc gcc cgc ggg ctg cgc gat ctg	816
Asp Ala Ala Phe Thr Tyr Ala Ala Ile Ala Arg Gly Leu Arg Asp Leu	
260 265 270	
 ggc aac cag cag tcg ccg ttc gac gcc tgg cag acc ctc cag aag ctc	864
Gly Asn Gln Gln Ser Pro Phe Asp Ala Trp Gln Thr Leu Gln Lys Leu	
275 280 285	

gaa acg ctc ccg ctg cgc atg caa caa cac tgc cgg aac gcc cag ctc 912
 Glu Thr Leu Pro Leu Arg Met Gln Gln His Cys Arg Asn Ala Gln Leu
 290 295 300

gtc gcc gaa cac ctc cgg gac cac ccc aac gtg tcg tgg gtc aac tac 960
 Val Ala Glu His Leu Arg Asp His Pro Asn Val Ser Trp Val Asn Tyr
 305 310 315 320

ccc ggg ctg gcc gac cac gac acc cac gac aac gca acc acc tac ctc 1008
 Pro Gly Leu Ala Asp His Asp Thr His Asp Asn Ala Thr Thr Tyr Leu
 325 330 335

gat tcg ggc tac gga ggc atg ctc acg ttc ggc gtc gag gac ggc tac 1056
 Asp Ser Gly Tyr Gly Gly Met Leu Thr Phe Gly Val Glu Asp Gly Tyr
 340 345 350

gag gcc gcc caa tcg gtc acc gag gag acc acg ctt gcc agc ctg ctg 1104
 Glu Ala Ala Gln Ser Val Thr Glu Glu Thr Thr Leu Ala Ser Leu Leu
 355 360 365

gcg aac gtc ggc gac gcc aaa acg ctc gtg atc cac ccc gcc tcc acc 1152
 Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser Thr
 370 375 380

acc cac cag cag ctc acc ccc gaa gcc cag cgc gcc ggc ggt gtg cgc 1200
 Thr His Gln Gln Leu Thr Pro Glu Ala Gln Arg Ala Gly Gly Val Arg
 385 390 395 400

ccc gag atg gtg cgg gtg tcg gtc ggc atc gag gac ccc gcc gac atc 1248
 Pro Glu Met Val Arg Val Ser Val Gly Ile Glu Asp Pro Ala Asp Ile
 405 410 415

gtc gcg gac ctc gaa acc gcc atc gag gcc gcg gtc ggg tcg gcg 1293
 Val Ala Asp Leu Glu Thr Ala Ile Glu Ala Ala Val Gly Ser Ala
 420 425 430

tag 1296

<210> 26

<211> 431

<212> PRT

<213> Halobacterium sp

<400> 26

Met Gly His Asp His Gly Leu His Thr Asn Ser Val His Ala Gly Gln
 1 5 10 15

Arg Val Asp Pro Ala Thr Gly Ala Arg Ala Pro Pro Leu Tyr Gln Thr
 20 25 30

Thr Ser Tyr Ala Phe Glu Asp Ser Ala Asp Ala Ala Gly Gln Phe Ala
 35 40 45

Leu Glu Arg Asp Gly Tyr Ile Tyr Ser Arg Leu Met Asn Pro Thr Val
 50 55 60

Glu Thr Leu Gln Asp Arg Leu Ala Ala Leu Glu Gly Gly Val Gly Ala
 65 70 75 80

Val Ala Thr Ala Ser Gly Met Ala Ala Leu Asp Leu Ala Thr Phe Leu
 85 90 95
 Leu Ala Arg Ala Gly Asp Ser Val Val Ala Ala Ser Asp Leu Tyr Gly
 100 105 110
 Gly Thr Val Thr Tyr Leu Thr His Ser Ala Gln Arg Arg Gly Val Asp
 115 120 125
 Thr Thr Phe Val Asp Val Leu Asp Tyr Asp Ala Tyr Ala Asp Ala Ile
 130 135 140
 Asp Ala Asp Thr Ala Tyr Val Leu Val Glu Thr Val Gly Asn Pro Ser
 145 150 155 160
 Leu Ile Thr Pro Asp Leu Glu Arg Ile Ala Asp Ile Ala His Asp Asn
 165 170 175
 Gly Val Pro Leu Leu Val Asp Asn Thr Phe Ala Thr Pro Ala Leu Ala
 180 185 190
 Thr Pro Ile Asp His Gly Ala Asp Ile Val Trp His Ser Thr Thr Lys
 195 200 205
 Trp Ile His Gly Ala Gly Thr Thr Val Gly Gly Ala Leu Val Asp Ala
 210 215 220
 Gly Ser Phe Asp Trp Asp Ala His Ala Ala Asp Tyr Pro Glu Ile Ala
 225 230 235 240
 Gln Glu Asn Pro Ala Tyr His Gly Val Thr Phe Thr Asp Arg Phe Gly
 245 250 255
 Asp Ala Ala Phe Thr Tyr Ala Ala Ile Ala Arg Gly Leu Arg Asp Leu
 260 265 270
 Gly Asn Gln Gln Ser Pro Phe Asp Ala Trp Gln Thr Leu Gln Lys Leu
 275 280 285
 Glu Thr Leu Pro Leu Arg Met Gln Gln His Cys Arg Asn Ala Gln Leu
 290 295 300
 Val Ala Glu His Leu Arg Asp His Pro Asn Val Ser Trp Val Asn Tyr
 305 310 315 320
 Pro Gly Leu Ala Asp His Asp Thr His Asp Asn Ala Thr Thr Tyr Leu
 325 330 335
 Asp Ser Gly Tyr Gly Gly Met Leu Thr Phe Gly Val Glu Asp Gly Tyr
 340 345 350
 Glu Ala Ala Gln Ser Val Thr Glu Glu Thr Thr Leu Ala Ser Leu Leu
 355 360 365
 Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser Thr
 370 375 380
 Thr His Gln Gln Leu Thr Pro Glu Ala Gln Arg Ala Gly Gly Val Arg
 385 390 395 400

Pro Glu Met Val Arg Val Ser Val Gly Ile Glu Asp Pro Ala Asp Ile
 405 410 415

Val Ala Asp Leu Glu Thr Ala Ile Glu Ala Ala Val Gly Ser Ala
 420 425 430

<210> 27
 <211> 1143
 <212> DNA
 <213> *Thermus thermophilus*

<220>
 <221> CDS
 <222> (1)..(1140)
 <223> RTT00268

<400> 27
 atg agc gag atc gcc ctc gag gcc tgg ggg gag cac gag gcc ctc ctc 48
 Met Ser Glu Ile Ala Leu Glu Ala Trp Gly Glu His Glu Ala Leu Leu
 1 5 10 15
 ctc aag ccc ccc cgc tcc ccc ctc tcc atc ccc ccg ccc aag ccc cgc 96
 Leu Lys Pro Pro Arg Ser Pro Leu Ser Ile Pro Pro Pro Lys Pro Arg
 20 25 30
 acc gcc gtc ctc ttc ccc agg cgg gag ggg ttc tac acg gag ctc ggg 144
 Thr Ala Val Leu Phe Pro Arg Arg Glu Gly Phe Tyr Thr Glu Leu Gly
 35 40 45
 ggg tac ctc ccc gag gtg cgc ctc cgc ttt gag acc tac ggg acc ctc 192
 Gly Tyr Leu Pro Glu Val Arg Leu Arg Phe Glu Thr Tyr Gly Thr Leu
 50 55 60
 tcc cgc agg cgg gat aac gcc gtc ctc gtc ttc cac gcc ctc acg ggg 240
 Ser Arg Arg Arg Asp Asn Ala Val Leu Val Phe His Ala Leu Thr Gly
 65 70 75 80
 agc gcc cac ctg gcg ggg acc tac gac gag gaa acc ttt aga agc ctc 288
 Ser Ala His Leu Ala Gly Thr Tyr Asp Glu Glu Thr Phe Arg Ser Leu
 85 90 95
 tcc ccc ctg gag cag gcc ttc ggc cgg gaa ggg tgg tgg gac agc ctg 336
 Ser Pro Leu Glu Gln Ala Phe Gly Arg Glu Gly Trp Trp Asp Ser Leu
 100 105 110
 gtg ggg ccc ggg cgg atc ctg gac ccc gcc ctc tac tac gtg gtc tcc 384
 Val Gly Pro Gly Arg Ile Leu Asp Pro Ala Leu Tyr Tyr Val Val Ser
 115 120 125
 gcc aac cac ctg gga agc tgc tac ggc tcc acc ggc ccc ctc tcc cta 432
 Ala Asn His Leu Gly Ser Cys Tyr Gly Ser Thr Gly Pro Leu Ser Leu
 130 135 140
 gac ccc cac acg ggc cgc ccc tac ggg agg gac ttc cct ccc ctt acc 480
 Asp Pro His Thr Gly Arg Pro Tyr Gly Arg Asp Phe Pro Pro Leu Thr
 145 150 155 160
 atc cgc gac ctg gcc cgg gcc cag gcg agg ctt ctg gac cat ctg ggg 528
 Ile Arg Asp Leu Ala Arg Ala Gln Ala Arg Leu Leu Asp His Leu Gly

165	170	175	
gtg gag aag gcc atc gtc atc ggg ggg agc ctc ggg ggg atg gtg gcc Val Glu Lys Ala Ile Val Ile Gly Gly Ser Leu Gly Gly Met Val Ala 180 185 190			576
ctg gag ttc gcc ctc atg tac ccg gag agg gtg aag aag ctc gtg gtc Leu Glu Phe Ala Leu Met Tyr Pro Glu Arg Val Lys Lys Leu Val Val 195 200 205			624
ctg gcg gcc ccc gca cgg cac ggc ccc tgg gcc cgg gcc ttc aac cac Leu Ala Ala Pro Ala Arg His Gly Pro Trp Ala Arg Ala Phe Asn His 210 215 220			672
ctc tcc cgc cag gcc atc ctc caa gac ccc gag tac cag aag ggc aac Leu Ser Arg Gln Ala Ile Leu Gln Asp Pro Glu Tyr Gln Lys Gly Asn 225 230 235 240			720
cct gcc ccc aag ggc atg gcc ctc gcc cgg gga atc gcc atg atg agc Pro Ala Pro Lys Gly Met Ala Leu Ala Arg Gly Ile Ala Met Met Ser 245 250 255			768
tac cgg gcc ccc gag ggg ttt gag gcc cgc tgg ggc gcg gag ccc gag Tyr Arg Ala Pro Glu Gly Phe Glu Ala Arg Trp Gly Ala Glu Pro Glu 260 265 270			816
ctc ggg gaa atc cac ctg gac tac cag ggg gag aag ttc ctc cgg cgc Leu Gly Glu Ile His Leu Asp Tyr Gln Gly Glu Lys Phe Leu Arg Arg 275 280 285			864
ttc cac gcc gag agc tac ctc gtc ctc tcc cgg gcc atg gac aac cac Phe His Ala Glu Ser Tyr Leu Val Leu Ser Arg Ala Met Asp Asn His 290 295 300			912
gac gtg ggc cgg ggc cgg ggc ggg gtg gag gag gcc ctg aag cgc ctc Asp Val Gly Arg Gly Arg Gly Gly Val Glu Glu Ala Leu Lys Arg Leu 305 310 315 320			960
agg gcc atc ccc tcc ctc ttc gtg ggc att gac acc gac ctc ctc tac Arg Ala Ile Pro Ser Leu Phe Val Gly Ile Asp Thr Asp Leu Leu Tyr 325 330 335			1008
ccc gcc tgg gag gtg agg cag gcg gcc aag gcg gcg ggg gcc cgc tac Pro Ala Trp Glu Val Arg Gln Ala Ala Lys Ala Ala Gly Ala Arg Tyr 340 345 350			1056
cgg gag atc aaa agc ccc cac ggg cac gac gcc ttc ctc ata gag acc Arg Glu Ile Lys Ser Pro His Gly His Asp Ala Phe Leu Ile Glu Thr 355 360 365			1104
gac cag gtg gag gag atc ctg gac gcc ttc ctc ccg tag Asp Gln Val Glu Glu Ile Leu Asp Ala Phe Leu Pro 370 375 380			1143

<210> 28

<211> 380

<212> PRT

<213> Thermus thermophilus

<400> 28

Met Ser Glu Ile Ala Leu Glu Ala Trp Gly Glu His Glu Ala Leu Leu
 1 5 10 15
 Leu Lys Pro Pro Arg Ser Pro Leu Ser Ile Pro Pro Pro Lys Pro Arg
 20 25 30
 Thr Ala Val Leu Phe Pro Arg Arg Glu Gly Phe Tyr Thr Glu Leu Gly
 35 40 45
 Gly Tyr Leu Pro Glu Val Arg Leu Arg Phe Glu Thr Tyr Gly Thr Leu
 50 55 60
 Ser Arg Arg Arg Asp Asn Ala Val Leu Val Phe His Ala Leu Thr Gly
 65 70 75 80
 Ser Ala His Leu Ala Gly Thr Tyr Asp Glu Glu Thr Phe Arg Ser Leu
 85 90 95
 Ser Pro Leu Glu Gln Ala Phe Gly Arg Glu Gly Trp Trp Asp Ser Leu
 100 105 110
 Val Gly Pro Gly Arg Ile Leu Asp Pro Ala Leu Tyr Tyr Val Val Ser
 115 120 125
 Ala Asn His Leu Gly Ser Cys Tyr Gly Ser Thr Gly Pro Leu Ser Leu
 130 135 140
 Asp Pro His Thr Gly Arg Pro Tyr Gly Arg Asp Phe Pro Pro Leu Thr
 145 150 155 160
 Ile Arg Asp Leu Ala Arg Ala Gln Ala Arg Leu Leu Asp His Leu Gly
 165 170 175
 Val Glu Lys Ala Ile Val Ile Gly Gly Ser Leu Gly Gly Met Val Ala
 180 185 190
 Leu Glu Phe Ala Leu Met Tyr Pro Glu Arg Val Lys Lys Leu Val Val
 195 200 205
 Leu Ala Ala Pro Ala Arg His Gly Pro Trp Ala Arg Ala Phe Asn His
 210 215 220
 Leu Ser Arg Gln Ala Ile Leu Gln Asp Pro Glu Tyr Gln Lys Gly Asn
 225 230 235 240
 Pro Ala Pro Lys Gly Met Ala Leu Ala Arg Gly Ile Ala Met Met Ser
 245 250 255
 Tyr Arg Ala Pro Glu Gly Phe Glu Ala Arg Trp Gly Ala Glu Pro Glu
 260 265 270
 Leu Gly Glu Ile His Leu Asp Tyr Gln Gly Glu Lys Phe Leu Arg Arg
 275 280 285
 Phe His Ala Glu Ser Tyr Leu Val Leu Ser Arg Ala Met Asp Asn His
 290 295 300
 Asp Val Gly Arg Gly Arg Gly Gly Val Glu Glu Ala Leu Lys Arg Leu
 305 310 315 320

Arg Ala Ile Pro Ser Leu Phe Val Gly Ile Asp Thr Asp Leu Leu Tyr
 325 330 335

Pro Ala Trp Glu Val Arg Gln Ala Ala Lys Ala Ala Gly Ala Arg Tyr
 340 345 350

Arg Glu Ile Lys Ser Pro His Gly His Asp Ala Phe Leu Ile Glu Thr
 355 360 365

Asp Gln Val Glu Glu Ile Leu Asp Ala Phe Leu Pro
 370 375 380

<210> 29

<211> 1005

<212> DNA

<213> Deinococcus radiodurans

<220>

<221> CDS

<222> (1) .. (1002)

<223> RDR01287

<400> 29

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 Val Thr Ala Val Leu Ala Gly His Ala Ser Ala Leu Leu Leu Thr Glu
 1 5 10 15

gaa ccc gac tgt tct ggg ccg cag acg gtc gtt ctc ttc cgg cgt gag 96
 Glu Pro Asp Cys Ser Gly Pro Gln Thr Val Val Leu Phe Arg Arg Glu
 20 25 30

ccg ctg ctg ctc gac tgc gga cgg gcg ctg agc gac gtg cgg gtg gcc 144
 Pro Leu Leu Leu Asp Cys Gly Arg Ala Leu Ser Asp Val Arg Val Ala
 35 40 45

ttt cac acc tac ggc acg ccg cgc gcc gac gcc acg ctg gtg ctg cac 192
 Phe His Thr Tyr Gly Thr Pro Arg Ala Asp Ala Thr Leu Val Leu His
 50 55 60

gcc ctg acc ggc gac agc gcg gtg cac gag tgg tgg ccc gac ttt ctg 240
 Ala Leu Thr Gly Asp Ser Ala Val His Glu Trp Trp Pro Asp Phe Leu
 65 70 75 80

ggc gcg ggc cgg cca ctg gac ccg gca gac gac tac gtg gtg tgc gcc 288
 Gly Ala Gly Arg Pro Leu Asp Pro Ala Asp Asp Tyr Val Val Cys Ala
 85 90 95

aac gtc ctc ggc ggg tgc gcc ggc acg acg agc gcc gct gaa ctc gcc 336
 Asn Val Leu Gly Gly Cys Ala Gly Thr Thr Ser Ala Ala Glu Leu Ala
 100 105 110

gcc acc tgt tcc gga ccg gtg ccg ctc agc ctg cgc gac atg gcc cgg 384
 Ala Thr Cys Ser Gly Pro Val Leu Ser Leu Arg Asp Met Ala Arg
 115 120 125

gtg ggg cgc gcc ctg ctg gat tct ctc ggc gtg cga cgg gtg cgg gtc 432
 Val Gly Arg Ala Leu Leu Asp Ser Leu Gly Val Arg Arg Val Arg Val
 130 135 140

atc ggc gcg agc atg ggc ggg atg ctc gcc tac gcc tgg ctg ctg gag 480
 Ile Gly Ala Ser Met Gly Gly Met Leu Ala Tyr Ala Trp Leu Leu Glu
 145 150 155 160

tgc ccc gac ctg gtg gaa aag gcc gtg att ata gga gcc ccg gcg cgg 528
 Cys Pro Asp Leu Val Glu Lys Ala Val Ile Ile Gly Ala Pro Ala Arg
 165 170 175

cac tcg ccc tgg gct att gga ctg aac acg gcg gcc cgc agc gcc att 576
 His Ser Pro Trp Ala Ile Gly Leu Asn Thr Ala Ala Arg Ser Ala Ile
 180 185 190

gcc ctc gct ccc ggc ggc gag ggg ctg aag gtg gcg cgc cag att gcc 624
 Ala Leu Ala Pro Gly Gly Glu Gly Leu Lys Val Ala Arg Gln Ile Ala
 195 200 205

atg ctc agt tac cgc agc ccc gaa agc cta agc cgc acg cag gcg ggg 672
 Met Leu Ser Tyr Arg Ser Pro Glu Ser Leu Ser Arg Thr Gln Ala Gly
 210 215 220

cag cgc gtg ccg ggg gtg ccc gcc gtt acg tct tac ctg cac tac caa 720
 Gln Arg Val Pro Gly Val Pro Ala Val Thr Ser Tyr Leu His Tyr Gln
 225 230 235 240

ggc gaa aaa ctc gcc gcc cgc ttc gac gag cag acc tac tgc gcc ctc 768
 Gly Glu Lys Leu Ala Ala Arg Phe Asp Glu Gln Thr Tyr Cys Ala Leu
 245 250 255

acc tgg gcg atg gac gcc ttt cag ccg agc agc gcc gac ctc aaa gcg 816
 Thr Trp Ala Met Asp Ala Phe Gln Pro Ser Ser Ala Asp Leu Lys Ala
 260 265 270

gtg cgc gcg ccg gta ctc gtc gtc ggc atc tcc agc gat ctg ctc tac 864
 Val Arg Ala Pro Val Leu Val Val Gly Ile Ser Ser Asp Leu Leu Tyr
 275 280 285

ccc gcc gcc gag gtc cgc gcc tgc gcc gcc gag ctt ccc cac gcc gac 912
 Pro Ala Ala Glu Val Arg Ala Cys Ala Ala Glu Leu Pro His Ala Asp
 290 295 300

tac tgg gaa ctg ggc agc att cac ggc cac gac gcc ttt ttg atg gac 960
 Tyr Trp Glu Leu Gly Ser Ile His Gly His Asp Ala Phe Leu Met Asp
 305 310 315 320

cca cag gac ttg ccg gag cgg gtg ggg gcg ttt ctc agg agt 1002
 Pro Gln Asp Leu Pro Glu Arg Val Gly Ala Phe Leu Arg Ser
 325 330

tga 1005

<210> 30

<211> 334

<212> PRT

<213> Deinococcus radiodurans

<400> 30

Val Thr Ala Val Leu Ala Gly His Ala Ser Ala Leu Leu Leu Thr Glu

1

5

10

15

Glu Pro Asp Cys Ser Gly Pro Gln Thr Val Val Leu Phe Arg Arg Glu
 20 25 30
 Pro Leu Leu Leu Asp Cys Gly Arg Ala Leu Ser Asp Val Arg Val Ala
 35 40 45
 Phe His Thr Tyr Gly Thr Pro Arg Ala Asp Ala Thr Leu Val Leu His
 50 55 60
 Ala Leu Thr Gly Asp Ser Ala Val His Glu Trp Trp Pro Asp Phe Leu
 65 70 75 80
 Gly Ala Gly Arg Pro Leu Asp Pro Ala Asp Asp Tyr Val Val Cys Ala
 85 90 95
 Asn Val Leu Gly Gly Cys Ala Gly Thr Thr Ser Ala Ala Glu Leu Ala
 100 105 110
 Ala Thr Cys Ser Gly Pro Val Pro Leu Ser Leu Arg Asp Met Ala Arg
 115 120 125
 Val Gly Arg Ala Leu Leu Asp Ser Leu Gly Val Arg Arg Val Arg Val
 130 135 140
 Ile Gly Ala Ser Met Gly Gly Met Leu Ala Tyr Ala Trp Leu Leu Glu
 145 150 155 160
 Cys Pro Asp Leu Val Glu Lys Ala Val Ile Ile Gly Ala Pro Ala Arg
 165 170 175
 His Ser Pro Trp Ala Ile Gly Leu Asn Thr Ala Ala Arg Ser Ala Ile
 180 185 190
 Ala Leu Ala Pro Gly Gly Glu Gly Leu Lys Val Ala Arg Gln Ile Ala
 195 200 205
 Met Leu Ser Tyr Arg Ser Pro Glu Ser Leu Ser Arg Thr Gln Ala Gly
 210 215 220
 Gln Arg Val Pro Gly Val Pro Ala Val Thr Ser Tyr Leu His Tyr Gln
 225 230 235 240
 Gly Glu Lys Leu Ala Ala Arg Phe Asp Glu Gln Thr Tyr Cys Ala Leu
 245 250 255
 Thr Trp Ala Met Asp Ala Phe Gln Pro Ser Ser Ala Asp Leu Lys Ala
 260 265 270
 Val Arg Ala Pro Val Leu Val Val Gly Ile Ser Ser Asp Leu Leu Tyr
 275 280 285
 Pro Ala Ala Glu Val Arg Ala Cys Ala Ala Glu Leu Pro His Ala Asp
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 Pro Gln Asp Leu Pro Glu Arg Val Gly Ala Phe Leu Arg Ser
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 <213> *Saccharomyces cerevisiae*

<220>
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 <222> (1)..(1458)
 <223> RSC08123

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 Glu Ile Lys Glu Thr Asn Pro Leu Leu Lys Leu Val Gln Gly Gln Arg
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 att gtt caa gtt ccg gaa cta gtg ctt gag tct ggc gtg gtc ata aat 144
 Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn
 35 40 45
 aat ttc cct att gct tat aag acg tgg ggt aca ctg aat gaa gct ggt 192
 Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly
 50 55 60
 gat aat gtt ctg gta att tgt cat gcc ttg act ggg tcc gca gat gtt 240
 Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val
 65 70 75 80
 gct gac tgg tgg ggc cct ctt ctg ggt aac gac tta gca ttc gac cca 288
 Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro
 85 90 95
 tca agg ttt ttt atc ata tgt tta aac tct atg ggc tct cca tat ggg 336
 Ser Arg Phe Phe Ile Ile Cys Leu Asn Ser Met Gly Ser Pro Tyr Gly
 100 105 110
 tct ttt tcg cca tta acg ata aat gag gag acg ggc gtt aga tat gga 384
 Ser Phe Ser Pro Leu Thr Ile Asn Glu Glu Thr Gly Val Arg Tyr Gly
 115 120 125
 ccc gaa ttc cca tta tgt act gtg cgc gat gac gtt aga gct cac aga 432
 Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg
 130 135 140
 att gtt ctg gat tct ctg gga gta aag tca ata gcc tgt gtt att ggt 480
 Ile Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys Val Ile Gly
 145 150 155 160
 ggc tct atg ggg ggg atg ctg agt ttg gaa tgg gct gcc atg tat ggt 528
 Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly
 165 170 175
 aag gaa tat gtg aag aat atg gtt gct ctg gcg aca tca gca aga cat 576
 Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His
 180 185 190

tct gcc tgg tgc ata tcg tgg tct gag gct caa aga caa tcg att tac	624
Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr	
195 200 205	
tca gat ccc aac tac ttg gac ggg tac tat ccg gta gag gag caa cct	672
Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro	
210 215 220	
gtg gcc gga cta tcg gct gca cgt atg tct gca ttg ttg acg tac agg	720
Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg	
225 230 235 240	
aca aga aac agt ttc gag aac aaa ttc tcc aga aga tct cct tca ata	768
Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile	
245 250 255	
gca caa caa caa aaa gct caa agg gag gag aca cgc aaa cca tct act	816
Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr	
260 265 270	
gtc agc gaa cac tcc cta caa atc cac aat gat ggg tat aaa aca aaa	864
Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys	
275 280 285	
gcc agc act gcc atc gct ggc att tct ggg caa aaa ggt caa agc gtg	912
Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val	
290 295 300	
gtg tcc acc gca tct tct tcg gat tca ttg aat tct tca aca tcg atg	960
Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met	
305 310 315 320	
act tcg gta agt tct gta acg ggt gaa gtg aag gac ata aag cct gcg	1008
Thr Ser Val Ser Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala	
325 330 335	
cag acg tat ttt tct gca caa agt tac ttg agg tac cag ggc aca aag	1056
Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys	
340 345 350	
ttc atc aat agg ttc gac gcc aat tgt tac att gcc atc aca cgt aaa	1104
Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys	
355 360 365	
ctg gat acg cac gat ttg gca aga gac aga gta gat gac atc act gag	1152
Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu	
370 375 380	
gtc ctt tct acc atc caa caa cca tcc ctg atc atc ggt atc caa tct	1200
Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser	
385 390 395 400	
gat gga ctg ttc aca tat tca gaa caa gaa ttt ttg gct gag cac ata	1248
Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile	
405 410 415	
ccg aag tcg caa tta gaa aaa att gaa tct ccc gaa ggc cac gat gcc	1296
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Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn
      35             40             45
Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly
  50             55             60
Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val
  65             70             75             80
Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro
          85             90             95
Ser Arg Phe Phe Ile Ile Cys Leu Asn Ser Met Gly Ser Pro Tyr Gly
          100             105             110
Ser Phe Ser Pro Leu Thr Ile Asn Glu Glu Thr Gly Val Arg Tyr Gly
      115             120             125
Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg
      130             135             140
Ile Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys Val Ile Gly
  145             150             155             160
Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly
          165             170             175
Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His
          180             185             190

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Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr
 195 200 205
 Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro
 210 215 220
 Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg
 225 230 235 240
 Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile
 245 250 255
 Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr
 260 265 270
 Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys
 275 280 285
 Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val
 290 295 300
 Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met
 305 310 315 320
 Thr Ser Val Ser Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala
 325 330 335
 Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys
 340 345 350
 Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys
 355 360 365
 Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu
 370 375 380
 Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser
 385 390 395 400
 Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile
 405 410 415
 Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala
 420 425 430
 Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu
 435 440 445
 Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly
 450 455 460
 Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala
 465 470 475 480
 Glu Glu Val Thr Asn Trp
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<210> 33

<211> 1470

<212> DNA

<213> Schizosaccharomyces pombe

<220>

<221> CDS

<222> (1)..(1467)

<223> RSO01936

<400> 33

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cat ccg tct cag caa gaa aat aaa ttt gtt cag ctt att tca gat caa      96
His Pro Ser Gln Gln Glu Asn Lys Phe Val Gln Leu Ile Ser Asp Gln
                20                      25                      30

aaa att gca att gtt ccc aaa ttt acg ttg gag tgt ggc gac atc ctt      144
Lys Ile Ala Ile Val Pro Lys Phe Thr Leu Glu Cys Gly Asp Ile Leu
                35                      40                      45

tac gat gtt ccc gtt gcc ttc aag act tgg ggt act ttg aat aaa gaa      192
Tyr Asp Val Pro Val Ala Phe Lys Thr Trp Gly Thr Leu Asn Lys Glu
                50                      55                      60

gga aac aat tgt ctt ctt ctt tgt cat gct tta agt ggt tct gct gat      240
Gly Asn Asn Cys Leu Leu Leu Cys His Ala Leu Ser Gly Ser Ala Asp
  65                      70                      75                      80

gct gga gat tgg tgg ggt cct tta ctc ggt cct ggt cgt gcg ttt gat      288
Ala Gly Asp Trp Trp Gly Pro Leu Leu Gly Pro Gly Arg Ala Phe Asp
                85                      90                      95

cca tca cat ttc ttt atc gta tgc ctt aat tct ctt ggt agc cca tac      336
Pro Ser His Phe Phe Ile Val Cys Leu Asn Ser Leu Gly Ser Pro Tyr
                100                      105                      110

gga agc gcc tct cct gtt aca tgg aac gct gag act cat agt gtt tat      384
Gly Ser Ala Ser Pro Val Thr Trp Asn Ala Glu Thr His Ser Val Tyr
                115                      120                      125

ggg cca gaa ttt cct tta gca acc ata cgt gat gat gta aac atc cat      432
Gly Pro Glu Phe Pro Leu Ala Thr Ile Arg Asp Asp Val Asn Ile His
                130                      135                      140

aaa ctt att tta caa aga ttg ggt gta aag caa att gct atg gca gta      480
Lys Leu Ile Leu Gln Arg Leu Gly Val Lys Gln Ile Ala Met Ala Val
                145                      150                      155                      160

ggt ggc tcc atg ggt ggt atg ctg gtt ttg gag tgg gca ttt gat aag      528
Gly Gly Ser Met Gly Gly Met Leu Val Leu Glu Trp Ala Phe Asp Lys
                165                      170                      175

gaa ttt gtg cga tca att gtt ccc att tct acc tct ctt cgt cat tcc      576
Glu Phe Val Arg Ser Ile Val Pro Ile Ser Thr Ser Leu Arg His Ser
                180                      185                      190

gcg tgg tgc att agc tgg tct gaa gcg caa cgc cag agt ata tat tct      624
Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr Ser
                195                      200                      205

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gac cct aag ttt aat gat gga tac tac ggc ata gac gat cag cct gta	672
Asp Pro Lys Phe Asn Asp Gly Tyr Tyr Gly Ile Asp Asp Gln Pro Val	
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Ser Gly Leu Gly Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg Ser	
225 230 235 240	
aaa tgt tct ttc gaa cgt cgc ttt gcc cgt act gtt cct gat gcg tct	768
Lys Cys Ser Phe Glu Arg Arg Phe Ala Arg Thr Val Pro Asp Ala Ser	
245 250 255	
cgt cac ccc tat cca gat cgt tta ccc act cct ctc acg ccc agt aat	816
Arg His Pro Tyr Pro Asp Arg Leu Pro Thr Pro Leu Thr Pro Ser Asn	
260 265 270	
gca cat tgg gtc gtt cac aac gaa gga aac cgt aat cgc cgt gaa cga	864
Ala His Trp Val Val His Asn Glu Gly Asn Arg Asn Arg Glu Arg	
275 280 285	
cct tgt cga tcc aat gga tca tca cct act tct gaa agt gct tta aat	912
Pro Cys Arg Ser Asn Gly Ser Ser Pro Thr Ser Glu Ser Ala Leu Asn	
290 295 300	
tcc ccc gcc tct tct gtc tcg tct tta cct tct tta ggt gcc tct cag	960
Ser Pro Ala Ser Ser Val Ser Ser Leu Pro Ser Leu Gly Ala Ser Gln	
305 310 315 320	
act aca gac agt tct tcc ctt aac cag agt tcg tta tta aga cgt cct	1008
Thr Thr Asp Ser Ser Ser Leu Asn Gln Ser Ser Leu Leu Arg Arg Pro	
325 330 335	
gct aat act tac ttc tct gcg caa tcg tat tta cgt tac caa gcg aag	1056
Ala Asn Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Ala Lys	
340 345 350	
aag ttt gta agt cgc ttt gat gct aat tgt tac att tcg att act aaa	1104
Lys Phe Val Ser Arg Phe Asp Ala Asn Cys Tyr Ile Ser Ile Thr Lys	
355 360 365	
aag ttg gac acc cat gat att act cgt gga cgc ggt tca gac tct cct	1152
Lys Leu Asp Thr His Asp Ile Thr Arg Gly Arg Gly Ser Asp Ser Pro	
370 375 380	
aag gaa gtc atg aag gat ttg tct tta ccc gta ctc gta ctc ggt att	1200
Lys Glu Val Met Lys Asp Leu Ser Leu Pro Val Leu Val Leu Gly Ile	
385 390 395 400	
gaa agc gat ggt ctt ttc aca ttt gac gaa caa gtt gaa att gcc aaa	1248
Glu Ser Asp Gly Leu Phe Thr Phe Asp Glu Gln Val Glu Ile Ala Lys	
405 410 415	
tct ttt ccc aat gct acc ttg gaa aaa att att tcg gcc gaa ggc cac	1296
Ser Phe Pro Asn Ala Thr Leu Glu Lys Ile Ile Ser Ala Glu Gly His	
420 425 430	
gac ggt ttt ttg ctt gag ttt act caa gta aac tca cat att caa aaa	1344
Asp Gly Phe Leu Leu Glu Phe Thr Gln Val Asn Ser His Ile Gln Lys	
435 440 445	

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 450 455 460

gag cga ctt gat tcc caa gtt aat gat acc aac cgc gaa agc gtt ttt 1440
 Glu Arg Leu Asp Ser Gln Val Asn Asp Thr Asn Arg Glu Ser Val Phe
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<210> 34

<211> 489

<212> PRT

<213> Schizosaccharomyces pombe

<400> 34

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Lys Ile Ala Ile Val Pro Lys Phe Thr Leu Glu Cys Gly Asp Ile Leu
 35 40 45

Tyr Asp Val Pro Val Ala Phe Lys Thr Trp Gly Thr Leu Asn Lys Glu
 50 55 60

Gly Asn Asn Cys Leu Leu Leu Cys His Ala Leu Ser Gly Ser Ala Asp
 65 70 75 80

Ala Gly Asp Trp Trp Gly Pro Leu Leu Gly Pro Gly Arg Ala Phe Asp
 85 90 95

Pro Ser His Phe Phe Ile Val Cys Leu Asn Ser Leu Gly Ser Pro Tyr
 100 105 110

Gly Ser Ala Ser Pro Val Thr Trp Asn Ala Glu Thr His Ser Val Tyr
 115 120 125

Gly Pro Glu Phe Pro Leu Ala Thr Ile Arg Asp Asp Val Asn Ile His
 130 135 140

Lys Leu Ile Leu Gln Arg Leu Gly Val Lys Gln Ile Ala Met Ala Val
 145 150 155 160

Gly Gly Ser Met Gly Gly Met Leu Val Leu Glu Trp Ala Phe Asp Lys
 165 170 175

Glu Phe Val Arg Ser Ile Val Pro Ile Ser Thr Ser Leu Arg His Ser
 180 185 190

Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr Ser
 195 200 205

Asp Pro Lys Phe Asn Asp Gly Tyr Tyr Gly Ile Asp Asp Gln Pro Val

210	215	220
Ser Gly Leu Gly Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg Ser		
225	230	235 240
Lys Cys Ser Phe Glu Arg Arg Phe Ala Arg Thr Val Pro Asp Ala Ser		
	245	250 255
Arg His Pro Tyr Pro Asp Arg Leu Pro Thr Pro Leu Thr Pro Ser Asn		
	260	265 270
Ala His Trp Val Val His Asn Glu Gly Asn Arg Asn Arg Arg Glu Arg		
	275	280 285
Pro Cys Arg Ser Asn Gly Ser Ser Pro Thr Ser Glu Ser Ala Leu Asn		
	290	295 300
Ser Pro Ala Ser Ser Val Ser Ser Leu Pro Ser Leu Gly Ala Ser Gln		
305	310	315 320
Thr Thr Asp Ser Ser Ser Leu Asn Gln Ser Ser Leu Leu Arg Arg Pro		
	325	330 335
Ala Asn Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Ala Lys		
	340	345 350
Lys Phe Val Ser Arg Phe Asp Ala Asn Cys Tyr Ile Ser Ile Thr Lys		
	355	360 365
Lys Leu Asp Thr His Asp Ile Thr Arg Gly Arg Gly Ser Asp Ser Pro		
	370	375 380
Lys Glu Val Met Lys Asp Leu Ser Leu Pro Val Leu Val Leu Gly Ile		
385	390	395 400
Glu Ser Asp Gly Leu Phe Thr Phe Asp Glu Gln Val Glu Ile Ala Lys		
	405	410 415
Ser Phe Pro Asn Ala Thr Leu Glu Lys Ile Ile Ser Ala Glu Gly His		
	420	425 430
Asp Gly Phe Leu Leu Glu Phe Thr Gln Val Asn Ser His Ile Gln Lys		
	435	440 445
Phe Gln Lys Glu His Leu Ile Asp Ile Met Ser Gln Thr Asn Ser Phe		
	450	455 460
Glu Arg Leu Asp Ser Gln Val Asn Asp Thr Asn Arg Glu Ser Val Phe		
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Gly Glu Met Glu Asp Ile Thr Ser Trp		
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<210> 35

<211> 1113

<212> DNA

<213> Xylella almond

<220>

<221> CDS

<222> (1)..(1110)

<223> RXFX01562

<400> 35

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cca ttt gcg atg aag cgt ggc gga caa ctc cac cac gcc cgc atc gct	96
Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala	
20 25 30	
tac gaa aca tgg ggc cgc ctc aat gcc agc gcc acc aat gcc att ctg	144
Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu	
35 40 45	
atc atg cct ggc tta tca ccc aat gca cat gcc gca cac cat gac agc	192
Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser	
50 55 60	
aat gct gag cca ggc tgg tgg gag tca atg cta ggt cca ggc aaa ccc	240
Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro	
65 70 75 80	
atc gac aca gac cgt tgg ttc gtg atc tgt gtc aac tca ctt ggt agc	288
Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser	
85 90 95	
tgc aaa gga tcg act ggc cct gca tcg tac aac ccc atc acg cag gcc	336
Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala	
100 105 110	
atg tat cgt ttg gac ttt cca gca ctg tca atc gaa gac ggg gcc aac	384
Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn	
115 120 125	
tcc gca att gaa gtg gta cat gca ctg ggc atc aag caa ctt gcc agc	432
Ser Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser	
130 135 140	
ctg atc ggc aat tca atg ggc ggc atg acg gca ctg gcc atc ctg ctg	480
Leu Ile Gly Asn Ser Met Gly Gly Met Thr Ala Leu Ala Ile Leu Leu	
145 150 155 160	
tta cat cca gat ata gcc cgc agc cac atc aac atc tca ggc agc gcg	528
Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala	
165 170 175	
cag gca tta ccg ttt tcc atc gcc att cgc tcg cta caa cgc gag gcg	576
Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala	
180 185 190	
atc cgc ctg gac ccc cat tgg agg cag gga gac tac gac gac acc cac	624
Ile Arg Leu Asp Pro His Trp Arg Gln Gly Asp Tyr Asp Asp Thr His	
195 200 205	
tac ccg gaa tcg ggg cta cgc atc gca cgc aaa ctt ggg gtg atc acc	672
Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr	
210 215 220	

tac cgc tcc gcg ctg gaa tgg gac ggg cgt ttt ggc cgg gta cgc ttg 720
 Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
 225 230 235 240

gat tcg gac caa acc aac gac aca cca ttc gga ctg gaa ttc caa att 768
 Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
 245 250 255

gaa aac tac ttg gaa agc cat gca cac cgc ttc gtg cac acc ttc gac 816
 Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
 260 265 270

cca aac tgc tac ctg tac ctg agc cgc tcc atg gac tgg ttc gac gtg 864
 Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
 275 280 285

gcc gag tac gcc aat gga gac att ctt gcc ggg ctg gcc agg atc cga 912
 Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300

atc caa cgc gca ctc gcc atc ggt agc cat acc gac atc ctc ttt cca 960
 Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320

ata caa cag caa caa caa att gcc gaa ggg cta cgc cgt ggc ggt aca 1008
 Ile Gln Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
 325 330 335

cac gcc acc ttc ctg ggc ctt gac tca ccg cag ggg cat gat gcg ttc 1056
 His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350

ctt gtg gat atc gca aga ttt ggc cct cca gtg aag gaa ttt ctg gac 1104
 Leu Val Asp Ile Ala Arg Phe Gly Pro Pro Val Lys Glu Phe Leu Asp
 355 360 365

gaa ctg tga 1113
 Glu Leu
 370

<210> 36

<211> 370

<212> PRT

<213> Xylella almond

<400> 36

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 20 25 30

Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45

Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60

Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80
 Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95
 Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110
 Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125
 Ser Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Ala Leu Ala Ile Leu Leu
 145 150 155 160
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175
 Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190
 Ile Arg Leu Asp Pro His Trp Arg Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205
 Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220
 Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
 225 230 235 240
 Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
 245 250 255
 Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
 260 265 270
 Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
 275 280 285
 Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300
 Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320
 Ile Gln Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
 325 330 335
 His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350
 Leu Val Asp Ile Ala Arg Phe Gly Pro Pro Val Lys Glu Phe Leu Asp
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 Glu Leu
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 <212> DNA
 <213> Xylella oleander

<220>
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 <222> (1)..(1110)
 <223> RXFY01729

<400> 37
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 Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
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 cca ttt gcg atg aag cgt ggc gga caa ctc cac cac gcc cgc atc gct 96
 Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30
 tac gaa aca tgg ggc cgc ctc aat gcc agc gcc acc aat gcc att ctg 144
 Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45
 atc atg cct ggc tta tca ccc aat gca cat gcc gca cac cat gac agc 192
 Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60
 aat gct gag cca ggc tgg tgg gag tca atg cta ggt cca ggc aaa ccc 240
 Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80
 atc gac aca gac cgt tgg ttc gtg atc tgt gtc aac tca ctt ggt agc 288
 Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95
 tgc aaa gga tgc act ggc cct gca tgc tac aac ccc atc acg cag gcc 336
 Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110
 atg tat cgt ttg gac ttt cca gca ctg tca atc gaa gac ggg gcc aac 384
 Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125
 gcc gca att gaa gtg gta cat gca ctg ggc atc aag caa ctt gcc agc 432
 Ala Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140
 ctg atc ggc aat tca atg ggg ggc atg acg aca ctg gcc atc ctg ctg 480
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Thr Leu Ala Ile Leu Leu
 145 150 155 160
 tta cat cca gat att gcc cgc agc cac atc aac atc tca ggc agc gcg 528
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175
 cag gca tta ccg ttt tcc atc gcc att cgc tgc cta caa cgc gag gcg 576
 Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190

atc cgc ctg gac ccc cat tgg aag cag gga gac tac gac gac acc cac 624
 Ile Arg Leu Asp Pro His Trp Lys Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205

tac ccg gaa tgc ggg cta cgc atc gca cgc aaa ctc ggg gtg atc acc 672
 Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220

tac cgc tcc gcg ctg gaa tgg gac ggg cgt ttt ggc cgg gta cgc ttg 720
 Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
 225 230 235 240

gat tgc gac caa acc aac gac aca cca ttc gga ctg gaa ttc caa att 768
 Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
 245 250 255

gaa aac tac ttg gaa agc cat gca cac cgc ttc gtg cac acc ttc gac 816
 Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
 260 265 270

cca aac tgc tac ctg tac ctg agc cgc tcc atg gac tgg ttc gac gtg 864
 Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
 275 280 285

gcc gag tac gcc aat gga gac att ctt gcc ggg ctg gcc agg atc cga 912
 Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300

atc caa cgc gca ctt gcc atc ggt agc cat acc gac atc ctc ttt cca 960
 Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320

ata caa cag caa caa caa att gcc gaa ggg cta cgc cgt ggc ggt aca 1008
 Ile Gln Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
 325 330 335

cac gcc acc ttc ctg ggc ctt gac tca ccg cag gga cat gat gcg ttc 1056
 His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350

ctt gtg gat atc gca gga ttt ggc cct cca gtg aag gaa ttt ctg ggc 1104
 Leu Val Asp Ile Ala Gly Phe Gly Pro Pro Val Lys Glu Phe Leu Gly
 355 360 365

gaa ctg tga 1113
 Glu Leu
 370

<210> 38

<211> 370

<212> PRT

<213> Xylella oleander

<400> 38

Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
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Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30

Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45
 Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60
 Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80
 Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95
 Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110
 Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125
 Ala Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Thr Leu Ala Ile Leu Leu
 145 150 155 160
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175
 Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190
 Ile Arg Leu Asp Pro His Trp Lys Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205
 Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220
 Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
 225 230 235 240
 Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
 245 250 255
 Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
 260 265 270
 Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
 275 280 285
 Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300
 Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320
 Ile Gln Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
 325 330 335
 His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350

Leu Val Asp Ile Ala Gly Phe Gly Pro Pro Val Lys Glu Phe Leu Gly
 355 360 365

Glu Leu
 370

<210> 39
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 <212> DNA
 <213> Emericella nidulans

<220>
 <221> CDS
 <222> (1)..(1575)
 <223> REN00010

<400> 39
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 gcc gtg acc agg cgg cct ttt cga gtt gtc cag ccg gcc atc gcc tgt 96
 Ala Val Thr Arg Arg Pro Phe Arg Val Val Gln Pro Ala Ile Ala Cys
 20 25 30
 ccg tcc aac agc cgg tcg ttt aac cat tct cga tca tta cga tca acg 144
 Pro Ser Asn Ser Arg Ser Phe Asn His Ser Arg Ser Leu Arg Ser Thr
 35 40 45
 ggg tct cag tcc ccc gct cca tcc cca cgc gac tcc tcg aat ccc gcg 192
 Gly Ser Gln Ser Pro Ala Pro Ser Pro Arg Asp Ser Ser Asn Pro Ala
 50 55 60
 ctg tcc ttc cct tgc ctc gac gcc cag gag gcc aag tcc gct ctt ctt 240
 Leu Ser Phe Pro Cys Leu Asp Ala Gln Glu Ala Lys Ser Ala Leu Leu
 65 70 75 80
 tcc gcg cga tct ctt ggt tca ggc cct gaa ccc tcc tat acc gcc ggc 288
 Ser Ala Arg Ser Leu Gly Ser Gly Pro Glu Pro Ser Tyr Thr Ala Gly
 85 90 95
 cac cac gaa cga ttc cat tcc gac gaa ccg ctg ctc ctt gat tgg ggc 336
 His His Glu Arg Phe His Ser Asp Glu Pro Leu Leu Leu Asp Trp Gly
 100 105 110
 ggt ttg ctt cca gaa ttt gat atc gca tat gag aca tgg ggc cag ctg 384
 Gly Leu Leu Pro Glu Phe Asp Ile Ala Tyr Glu Thr Trp Gly Gln Leu
 115 120 125
 aac gag aag aag gat aat gtc att ctg ctg cat acc ggt ctg tct gca 432
 Asn Glu Lys Lys Asp Asn Val Ile Leu Leu His Thr Gly Leu Ser Ala
 130 135 140
 tct agc cat gcg cac agc acc gaa gcg aac ccg aag ccc ggc tgg tgg 480
 Ser Ser His Ala His Ser Thr Glu Ala Asn Pro Lys Pro Gly Trp Trp
 145 150 155 160
 gag aaa ttc ata ggt cct ggg aag acg cta gat acg gac aag tac ttt 528

Glu Lys Phe Ile Gly Pro Gly Lys Thr Leu Asp Thr Asp Lys Tyr Phe	
165 170 175	
gtg atc tgc acc aat gtc ctt gga ggg tgc tac ggt agc acg ggg ccc	576
Val Ile Cys Thr Asn Val Leu Gly Gly Cys Tyr Gly Ser Thr Gly Pro	
180 185 190	
tcg acg gtg gac ccg tcg gat ggg aag aag tat gct acg cgg ttt ccc	624
Ser Thr Val Asp Pro Ser Asp Gly Lys Lys Tyr Ala Thr Arg Phe Pro	
195 200 205	
atc ctg aca att gaa gat atg gtg cga gcg cag ttc cgc ctt ttg gac	672
Ile Leu Thr Ile Glu Asp Met Val Arg Ala Gln Phe Arg Leu Leu Asp	
210 215 220	
cat ctt ggg gtt cgg aaa ctc tac gcg tcc gtc ggc tcc agc atg ggt	720
His Leu Gly Val Arg Lys Leu Tyr Ala Ser Val Gly Ser Ser Met Gly	
225 230 235 240	
ggg atg cag agt ctt gca gcc ggt gtt ctg ttc cca gag cga gtg ggc	768
Gly Met Gln Ser Leu Ala Ala Gly Val Leu Phe Pro Glu Arg Val Gly	
245 250 255	
aag att gtg tcg att agc ggt tgt gct cga agc cat ccg tac agc att	816
Lys Ile Val Ser Ile Ser Gly Cys Ala Arg Ser His Pro Tyr Ser Ile	
260 265 270	
gct atg cgc cat acc cag cgg cag gtg ttg atg atg gat cca aat tgg	864
Ala Met Arg His Thr Gln Arg Gln Val Leu Met Met Asp Pro Asn Trp	
275 280 285	
gct cga ggt ttc tac tac gat tcg atc cca cct cat tca ggc atg aag	912
Ala Arg Gly Phe Tyr Tyr Asp Ser Ile Pro Pro His Ser Gly Met Lys	
290 295 300	
ctc gct cgc gag att gcc acc gtc acg tac cgc agc gga cca gaa tgg	960
Leu Ala Arg Glu Ile Ala Thr Val Thr Tyr Arg Ser Gly Pro Glu Trp	
305 310 315 320	
gag aaa cgc ttt ggt cgg aaa cgg gct gat ccg agc aaa cag cct gcg	1008
Glu Lys Arg Phe Gly Arg Lys Arg Ala Asp Pro Ser Lys Gln Pro Ala	
325 330 335	
ctt tgc ccc gac ttt ctc atc gag acg tat ctc gac cac gcc ggt gaa	1056
Leu Cys Pro Asp Phe Leu Ile Glu Thr Tyr Leu Asp His Ala Gly Glu	
340 345 350	
aaa ttc tgc ttg gaa tac gat gcc aac agc ctg ctc tac atc tcc aag	1104
Lys Phe Cys Leu Glu Tyr Asp Ala Asn Ser Leu Leu Tyr Ile Ser Lys	
355 360 365	
gcg atg gat ctg ttt gac cta ggg ttg act cag caa ctc gcg acg aag	1152
Ala Met Asp Leu Phe Asp Leu Gly Leu Thr Gln Gln Leu Ala Thr Lys	
370 375 380	
aag cag agg gcg gag gcc cag gcg aag att agc agc gga aca aac act	1200
Lys Gln Arg Ala Glu Ala Gln Ala Lys Ile Ser Ser Gly Thr Asn Thr	
385 390 395 400	
gtc aat gat gcg tcg tgc agc ctt aca ctt cct gaa cag cca tac cag	1248

Val Asn Asp Ala Ser Cys Ser Leu Thr Leu Pro Glu Gln Pro Tyr Gln
 405 410 415

gag cag cca tct gcc tcg aca tcc gcc gag cag tct gct tcc gct tca 1296
 Glu Gln Pro Ser Ala Ser Thr Ser Ala Glu Gln Ser Ala Ser Ala Ser
 420 425 430

gag acc ggg tcg gct ccg aac gat ctt gtt gcc ggg ctt gcg ccg ctg 1344
 Glu Thr Gly Ser Ala Pro Asn Asp Leu Val Ala Gly Leu Ala Pro Leu
 435 440 445

aaa gac cat cag gtg ctg gta atc gga gtc gca agc gac att ctc ttc 1392
 Lys Asp His Gln Val Leu Val Ile Gly Val Ala Ser Asp Ile Leu Phe
 450 455 460

ccg gcg tgg caa cag cgc gag atc gcg gag act ctg att caa gca ggg 1440
 Pro Ala Trp Gln Gln Arg Glu Ile Ala Glu Thr Leu Ile Gln Ala Gly
 465 470 475 480

aac aag acc gtg gag cat att gag ctg ggc aac gac gtg tct ctc ttt 1488
 Asn Lys Thr Val Glu His Ile Glu Leu Gly Asn Asp Val Ser Leu Phe
 485 490 495

ggt cat gac aca ttc ctc ctt gat gtc aga acg tcg gag gcg cag ttc 1536
 Gly His Asp Thr Phe Leu Leu Asp Val Arg Thr Ser Glu Ala Gln Phe
 500 505 510

gca agt tcc gta cta gtc ggc tcg cac ata att gta caa tag 1578
 Ala Ser Ser Val Leu Val Gly Ser His Ile Ile Val Gln
 515 520 525

<210> 40
 <211> 525
 <212> PRT
 <213> *Emericella nidulans*

<400> 40
 Met Ser Pro Leu Asn Gly Val Ala Arg Ser Phe Pro Arg Pro Phe Gln
 1 5 10 15

Ala Val Thr Arg Arg Pro Phe Arg Val Val Gln Pro Ala Ile Ala Cys
 20 25 30

Pro Ser Asn Ser Arg Ser Phe Asn His Ser Arg Ser Leu Arg Ser Thr
 35 40 45

Gly Ser Gln Ser Pro Ala Pro Ser Pro Arg Asp Ser Ser Asn Pro Ala
 50 55 60

Leu Ser Phe Pro Cys Leu Asp Ala Gln Glu Ala Lys Ser Ala Leu Leu
 65 70 75 80

Ser Ala Arg Ser Leu Gly Ser Gly Pro Glu Pro Ser Tyr Thr Ala Gly
 85 90 95

His His Glu Arg Phe His Ser Asp Glu Pro Leu Leu Leu Asp Trp Gly
 100 105 110

Gly Leu Leu Pro Glu Phe Asp Ile Ala Tyr Glu Thr Trp Gly Gln Leu

115		120		125
Asn Glu Lys Lys Asp Asn Val Ile Leu Leu His Thr Gly Leu Ser Ala				
130		135		140
Ser Ser His Ala His Ser Thr Glu Ala Asn Pro Lys Pro Gly Trp Trp				
145		150		155
				160
Glu Lys Phe Ile Gly Pro Gly Lys Thr Leu Asp Thr Asp Lys Tyr Phe				
		165		170
				175
Val Ile Cys Thr Asn Val Leu Gly Gly Cys Tyr Gly Ser Thr Gly Pro				
		180		185
				190
Ser Thr Val Asp Pro Ser Asp Gly Lys Lys Tyr Ala Thr Arg Phe Pro				
		195		200
				205
Ile Leu Thr Ile Glu Asp Met Val Arg Ala Gln Phe Arg Leu Leu Asp				
		210		215
				220
His Leu Gly Val Arg Lys Leu Tyr Ala Ser Val Gly Ser Ser Met Gly				
		225		230
				235
Gly Met Gln Ser Leu Ala Ala Gly Val Leu Phe Pro Glu Arg Val Gly				
		245		250
				255
Lys Ile Val Ser Ile Ser Gly Cys Ala Arg Ser His Pro Tyr Ser Ile				
		260		265
				270
Ala Met Arg His Thr Gln Arg Gln Val Leu Met Met Asp Pro Asn Trp				
		275		280
				285
Ala Arg Gly Phe Tyr Tyr Asp Ser Ile Pro Pro His Ser Gly Met Lys				
		290		295
				300
Leu Ala Arg Glu Ile Ala Thr Val Thr Tyr Arg Ser Gly Pro Glu Trp				
		305		310
				315
				320
Glu Lys Arg Phe Gly Arg Lys Arg Ala Asp Pro Ser Lys Gln Pro Ala				
		325		330
				335
Leu Cys Pro Asp Phe Leu Ile Glu Thr Tyr Leu Asp His Ala Gly Glu				
		340		345
				350
Lys Phe Cys Leu Glu Tyr Asp Ala Asn Ser Leu Leu Tyr Ile Ser Lys				
		355		360
				365
Ala Met Asp Leu Phe Asp Leu Gly Leu Thr Gln Gln Leu Ala Thr Lys				
		370		375
				380
Lys Gln Arg Ala Glu Ala Gln Ala Lys Ile Ser Ser Gly Thr Asn Thr				
		385		390
				395
				400
Val Asn Asp Ala Ser Cys Ser Leu Thr Leu Pro Glu Gln Pro Tyr Gln				
		405		410
				415
Glu Gln Pro Ser Ala Ser Thr Ser Ala Glu Gln Ser Ala Ser Ala Ser				
		420		425
				430
Glu Thr Gly Ser Ala Pro Asn Asp Leu Val Ala Gly Leu Ala Pro Leu				

435

440

445

Lys Asp His Gln Val Leu Val Ile Gly Val Ala Ser Asp Ile Leu Phe
 450 455 460

Pro Ala Trp Gln Gln Arg Glu Ile Ala Glu Thr Leu Ile Gln Ala Gly
 465 470 475 480

Asn Lys Thr Val Glu His Ile Glu Leu Gly Asn Asp Val Ser Leu Phe
 485 490 495

Gly His Asp Thr Phe Leu Leu Asp Val Arg Thr Ser Glu Ala Gln Phe
 500 505 510

Ala Ser Ser Val Leu Val Gly Ser His Ile Ile Val Gln
 515 520 525

<210> 41

<211> 1170

<212> DNA

<213> Mesorhizobium loti

<220>

<221> CDS

<222> (1)..(1167)

<223> NP_104621

<400> 41

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 Met Ala Ala Leu Arg Ala Gly Lys Thr Asn Asn Glu Ala Asp Gln Pro
 1 5 10 15

tcg agc ccg gtg ttg cgc ttc ggg gcg gac aag ccg ctc aag ctc gac 96
 Ser Ser Pro Val Leu Arg Phe Gly Ala Asp Lys Pro Leu Lys Leu Asp
 20 25 30

gcc ggc acg ctt ttg tcg ccg ttc cag atc gcc tat cag acc tac ggc 144
 Ala Gly Thr Leu Leu Ser Pro Phe Gln Ile Ala Tyr Gln Thr Tyr Gly
 35 40 45

acg ctg aac gat gcc cgc tcc aat gcc atc ctc gtc tgc cat gcg ctg 192
 Thr Leu Asn Asp Ala Arg Ser Asn Ala Ile Leu Val Cys His Ala Leu
 50 55 60

acc ggc gac cag cat gtc gcc aac acc aat ccg gtg acc ggc aag ccg 240
 Thr Gly Asp Gln His Val Ala Asn Thr Asn Pro Val Thr Gly Lys Pro
 65 70 75 80

gga tgg tgg gaa gtg ctg atc ggc ccc ggc agg atc atc gac acc aac 288
 Gly Trp Trp Glu Val Leu Ile Gly Pro Gly Arg Ile Ile Asp Thr Asn
 85 90 95

cgt ttc ttc gtc atc tgc tcc aac gtc atc ggc ggt tgt ctg ggc tcc 336
 Arg Phe Phe Val Ile Cys Ser Asn Val Ile Gly Gly Cys Leu Gly Ser
 100 105 110

acc ggc ccg gcc tcg acc aac ccc gcc acc ggc aag ccc tac ggg ctc 384
 Thr Gly Pro Ala Ser Thr Asn Pro Ala Thr Gly Lys Pro Tyr Gly Leu
 115 120 125

gac ctg ccg gtc atc acc atc cgc gat atg gtg cgc gcg cag cag atg	432
Asp Leu Pro Val Ile Thr Ile Arg Asp Met Val Arg Ala Gln Gln Met	
130 135 140	
ctg atc gat cat ttc ggc atc gag aaa ctg ttc tgc gtg ctc ggc ggc	480
Leu Ile Asp His Phe Gly Ile Glu Lys Leu Phe Cys Val Leu Gly Gly	
145 150 155 160	
tcg atg ggc gga atg cag gtg ctg gaa tgg gcg tcg agc tac ccc gag	528
Ser Met Gly Gly Met Gln Val Leu Glu Trp Ala Ser Ser Tyr Pro Glu	
165 170 175	
cgc gtc ttt tcg gca ctg ccg atc gcc acc ggc gcg cgc cat tcc tcg	576
Arg Val Phe Ser Ala Leu Pro Ile Ala Thr Gly Ala Arg His Ser Ser	
180 185 190	
cag aac atc gcc ttc cac gag gtc ggc cgg cag gct gtc atg gcc gat	624
Gln Asn Ile Ala Phe His Glu Val Gly Arg Gln Ala Val Met Ala Asp	
195 200 205	
ccg gac tgg cac ggc ggc aaa tat ttc gaa aac ggc aaa cgc ccg gaa	672
Pro Asp Trp His Gly Gly Lys Tyr Phe Glu Asn Gly Lys Arg Pro Glu	
210 215 220	
aag ggc ctg gcg gta gcg cgc atg gcc gcc cac ata acc tat ctg tcg	720
Lys Gly Leu Ala Val Ala Arg Met Ala Ala His Ile Thr Tyr Leu Ser	
225 230 235 240	
gaa gcc gcc ctg cac cgg aaa ttc ggc cgc aat ctg cag gat cgc gag	768
Glu Ala Ala Leu His Arg Lys Phe Gly Arg Asn Leu Gln Asp Arg Glu	
245 250 255	
gcg ctg acc ttc ggc ttc gac gcc gac ttc cag atc gaa agc tat ctg	816
Ala Leu Thr Phe Gly Phe Asp Ala Asp Phe Gln Ile Glu Ser Tyr Leu	
260 265 270	
cgc cac caa ggc atg acc ttc gtc gac cgc ttc gac gcc aat tcc tat	864
Arg His Gln Gly Met Thr Phe Val Asp Arg Phe Asp Ala Asn Ser Tyr	
275 280 285	
ctc tac atg acg cgg tcg atg gac tat ttc gac ctc gcc gcc gat cat	912
Leu Tyr Met Thr Arg Ser Met Asp Tyr Phe Asp Leu Ala Ala Asp His	
290 295 300	
ggc ggg cgg ctg gcg gat gcc ttt gcc ggc acc aaa acc cgc ttc tgc	960
Gly Gly Arg Leu Ala Asp Ala Phe Ala Gly Thr Lys Thr Arg Phe Cys	
305 310 315 320	
ctg gtg tcc ttc acc tcg gat tgg ttg ttt ccg acc gaa gag agc cgc	1008
Leu Val Ser Phe Thr Ser Asp Trp Leu Phe Pro Thr Glu Glu Ser Arg	
325 330 335	
tcg atc gtg cac gcg ctc aac gcc gcc ggc gcg tcc gtg tcc ttc gtc	1056
Ser Ile Val His Ala Leu Asn Ala Ala Gly Ala Ser Val Ser Phe Val	
340 345 350	
gaa atc gag acc gac cgc ggc cac gat gcc ttc ctg ctc gac gag ccg	1104
Glu Ile Glu Thr Asp Arg Gly His Asp Ala Phe Leu Leu Asp Glu Pro	
355 360 365	

gaa ctg ttc gcc gcc atc aac ggc ttc atc ggc tcc gcg gcg cgg gcg 1152
 Glu Leu Phe Ala Ala Ile Asn Gly Phe Ile Gly Ser Ala Ala Arg Ala
 370 375 380

aga ggg cta agc gca tga 1170
 Arg Gly Leu Ser Ala
 385

<210> 42
 <211> 389
 <212> PRT
 <213> Mesorhizobium loti

<400> 42
 Met Ala Ala Leu Arg Ala Gly Lys Thr Asn Asn Glu Ala Asp Gln Pro
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Ser Ser Pro Val Leu Arg Phe Gly Ala Asp Lys Pro Leu Lys Leu Asp
 20 25 30

Ala Gly Thr Leu Leu Ser Pro Phe Gln Ile Ala Tyr Gln Thr Tyr Gly
 35 40 45

Thr Leu Asn Asp Ala Arg Ser Asn Ala Ile Leu Val Cys His Ala Leu
 50 55 60

Thr Gly Asp Gln His Val Ala Asn Thr Asn Pro Val Thr Gly Lys Pro
 65 70 75 80

Gly Trp Trp Glu Val Leu Ile Gly Pro Gly Arg Ile Ile Asp Thr Asn
 85 90 95

Arg Phe Phe Val Ile Cys Ser Asn Val Ile Gly Gly Cys Leu Gly Ser
 100 105 110

Thr Gly Pro Ala Ser Thr Asn Pro Ala Thr Gly Lys Pro Tyr Gly Leu
 115 120 125

Asp Leu Pro Val Ile Thr Ile Arg Asp Met Val Arg Ala Gln Gln Met
 130 135 140

Leu Ile Asp His Phe Gly Ile Glu Lys Leu Phe Cys Val Leu Gly Gly
 145 150 155 160

Ser Met Gly Gly Met Gln Val Leu Glu Trp Ala Ser Ser Tyr Pro Glu
 165 170 175

Arg Val Phe Ser Ala Leu Pro Ile Ala Thr Gly Ala Arg His Ser Ser
 180 185 190

Gln Asn Ile Ala Phe His Glu Val Gly Arg Gln Ala Val Met Ala Asp
 195 200 205

Pro Asp Trp His Gly Gly Lys Tyr Phe Glu Asn Gly Lys Arg Pro Glu
 210 215 220

Lys Gly Leu Ala Val Ala Arg Met Ala Ala His Ile Thr Tyr Leu Ser
 225 230 235 240

Glu Ala Ala Leu His Arg Lys Phe Gly Arg Asn Leu Gln Asp Arg Glu
245 250 255

Ala Leu Thr Phe Gly Phe Asp Ala Asp Phe Gln Ile Glu Ser Tyr Leu
260 265 270

Arg His Gln Gly Met Thr Phe Val Asp Arg Phe Asp Ala Asn Ser Tyr
275 280 285

Leu Tyr Met Thr Arg Ser Met Asp Tyr Phe Asp Leu Ala Ala Asp His
290 295 300

Gly Gly Arg Leu Ala Asp Ala Phe Ala Gly Thr Lys Thr Arg Phe Cys
305 310 315 320

Leu Val Ser Phe Thr Ser Asp Trp Leu Phe Pro Thr Glu Glu Ser Arg
325 330 335

Ser Ile Val His Ala Leu Asn Ala Ala Gly Ala Ser Val Ser Phe Val
340 345 350

Glu Ile Glu Thr Asp Arg Gly His Asp Ala Phe Leu Leu Asp Glu Pro
355 360 365

Glu Leu Phe Ala Ala Ile Asn Gly Phe Ile Gly Ser Ala Ala Arg Ala
370 375 380

Arg Gly Leu Ser Ala
385

<210> 43

<211> 1155

<212> DNA

<213> acremonium crysogenum

<220>

<221> CDS

<222> (1)..(1152)

<223> P39058

<400> 43

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Cys Arg Leu Arg Ser Pro Ile Ala Ser Arg Leu Arg Xaa Met Pro Lys
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aca tag cca gaa tat cgc tct tca cac tgg aat ctg gcg tca tcc ttc 96
Thr Xaa Pro Glu Tyr Arg Ser Ser His Trp Asn Leu Ala Ser Ser Phe
20 25 30

gcg atg tac ccg tgg cat aca aat cgt ggg gtc gca tga atg tct caa 144
Ala Met Tyr Pro Trp His Thr Asn Arg Gly Val Ala Xaa Met Ser Gln
35 40 45

ggg ata act gcg tca tcg tct gcc aca cct tga cga gca gcg ccc atg 192
Gly Ile Thr Ala Ser Ser Ser Ala Thr Pro Xaa Arg Ala Ala Pro Met
50 55 60

tca cct cgt ggt ggc cca cac tgt ttg gcc aag gca ggg ctt tcg ata 240

Ser 65	Pro	Arg	Gly	Gly	Pro 70	His	Cys	Leu	Ala	Lys 75	Ala	Gly	Leu	Ser	Ile 80	
cct	ctc	gct	act	tca	tca	tct	gcc	taa	att	atc	tcg	gga	gcc	cct	ttg	288
Pro	Leu	Ala	Thr	Ser	Ser	Ser	Ala	Xaa	Ile	Ile	Ser	Gly	Ala	Pro	Leu	
				85					90					95		
gga	gtg	ctg	gac	cat	gtt	cac	cgg	acc	ccg	atg	cag	aag	gcc	agc	gcc	336
Gly	Val	Leu	Asp	His	Val	His	Arg	Thr	Pro	Met	Gln	Lys	Ala	Ser	Ala	
			100					105					110			
cgt	acg	ggg	cca	agt	ttc	ctc	gca	cga	cga	ttc	gag	atg	atg	ttc	gta	384
Arg	Thr	Gly	Pro	Ser	Phe	Leu	Ala	Arg	Arg	Phe	Glu	Met	Met	Phe	Val	
		115					120					125				
ttc	atc	gcc	agg	tgc	tcg	aca	ggt	tag	gcg	tca	ggc	aaa	ttg	ctg	ccg	432
Phe	Ile	Ala	Arg	Cys	Ser	Thr	Gly	Xaa	Ala	Ser	Gly	Lys	Leu	Leu	Pro	
	130					135					140					
tag	tcg	gcg	cat	cca	tgg	gtg	gaa	tgc	aca	ctc	tgg	aat	ggg	cct	tct	480
Xaa	Ser	Ala	His	Pro	Trp	Val	Glu	Cys	Thr	Leu	Trp	Asn	Gly	Pro	Ser	
145					150					155					160	
ttg	gtc	ccg	agt	acg	tgc	gaa	aga	ttg	tgc	cca	tcg	cga	cat	cat	gcc	528
Leu	Val	Pro	Ser	Thr	Cys	Glu	Arg	Leu	Cys	Pro	Ser	Arg	His	His	Ala	
				165					170					175		
gtc	aga	gcg	gct	ggt	gcg	cag	ctt	ggt	tcg	aga	cac	aga	ggc	agt	gca	576
Val	Arg	Ala	Ala	Gly	Ala	Gln	Leu	Gly	Ser	Arg	His	Arg	Gly	Ser	Ala	
			180					185					190			
tct	atg	atg	acc	cca	agt	acc	tgg	acg	ggg	agt	acg	acg	tag	acg	acc	624
Ser	Met	Met	Thr	Pro	Ser	Thr	Trp	Thr	Gly	Ser	Thr	Thr	Xaa	Thr	Thr	
		195					200					205				
agc	ctg	tcc	ggg	ggc	tcg	aaa	cag	cgc	gca	aga	ttg	cga	atc	tca	cgt	672
Ser	Leu	Ser	Gly	Gly	Ser	Lys	Gln	Arg	Ala	Arg	Leu	Arg	Ile	Ser	Arg	
	210					215					220					
aca	aga	gca	aac	ctg	cga	tgg	acg	agc	gct	tcc	ata	tgg	ctc	cag	gag	720
Thr	Arg	Ala	Asn	Leu	Arg	Trp	Thr	Ser	Ala	Ser	Ile	Trp	Leu	Gln	Glu	
225					230					235					240	
tcc	aag	ccg	gcc	gga	ata	tca	gca	gcc	agg	atg	cga	aga	agg	aaa	tca	768
Ser	Lys	Pro	Ala	Gly	Ile	Ser	Ala	Ala	Arg	Met	Arg	Arg	Arg	Lys	Ser	
			245						250					255		
acg	gca	cag	aca	gcg	gca	aca	gcc	acc	gtg	ctg	gcc	agc	cca	ttg	aag	816
Thr	Ala	Gln	Thr	Ala	Ala	Thr	Ala	Thr	Val	Leu	Ala	Ser	Pro	Leu	Lys	
			260					265					270			
ccg	tat	ctt	cct	atc	tcc	ggt	acc	agg	ccc	aga	agt	ttg	ccg	cga	gct	864
Pro	Tyr	Leu	Pro	Ile	Ser	Gly	Thr	Arg	Pro	Arg	Ser	Leu	Pro	Arg	Ala	
		275					280					285				
tcg	acg	cca	act	gct	aca	tcg	cca	tga	cac	tca	agt	tcg	aca	ccc	acg	912
Ser	Thr	Pro	Thr	Ala	Thr	Ser	Pro	Xaa	His	Ser	Ser	Ser	Thr	Pro	Thr	
	290					295					300					
aca	tca	gca	gag	gcc	ggg	cag	gat	caa	tcc	cgg	agg	ctc	tgg	caa	tga	960

Thr	Ser	Ala	Glu	Ala	Gly	Gln	Asp	Gln	Ser	Arg	Arg	Leu	Trp	Gln	Xaa	
305					310					315					320	
tta	cac	aac	cag	cgt	tga	tca	ttt	gcg	cca	ggc	cag	acg	gtc	tgt	act	1008
Leu	His	Asn	Gln	Arg	Xaa	Ser	Phe	Ala	Pro	Gly	Gln	Thr	Val	Cys	Thr	
			325						330					335		
cgt	ttg	acg	agc	acg	ttg	aga	tgg	ggc	gca	gta	tcc	caa	aca	gtc	gtc	1056
Arg	Leu	Thr	Ser	Thr	Leu	Arg	Trp	Gly	Ala	Val	Ser	Gln	Thr	Val	Val	
			340					345					350			
ttt	gcg	tgg	tgg	aca	cga	atg	agg	gtc	atg	act	tct	ttg	taa	tgg	aag	1104
Phe	Ala	Trp	Trp	Thr	Arg	Met	Arg	Val	Met	Thr	Ser	Leu	Xaa	Trp	Lys	
		355					360						365			
cgg	aca	agg	tta	atg	atg	cgc	tca	gag	gat	tcc	tcg	atc	agt	cat	taa	1152
Arg	Thr	Arg	Leu	Met	Met	Pro	Ser	Glu	Asp	Ser	Ser	Ile	Ser	His	Xaa	
		370				375					380					
tgt																1155

<210> 44
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 <213> acremonium crysogenum

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<220>
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<220>
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<221> unsure

<222> 206 .. 206

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<221> unsure

<222> 297 .. 297

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<221> unsure

<222> 320 .. 320

<223> All occurrences of Xaa indicate any amino acid

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<221> unsure

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<223> All occurrences of Xaa indicate any amino acid

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<222> 366 .. 366

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<222> 384 .. 384

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Ala	Met	Tyr	Pro	Trp	His	Thr	Asn	Arg	Gly	Val	Ala	Xaa	Met	Ser	Gln
	35						40					45			

Gly	Ile	Thr	Ala	Ser	Ser	Ser	Ala	Thr	Pro	Xaa	Arg	Ala	Ala	Pro	Met
	50					55					60				

Ser	Pro	Arg	Gly	Gly	Pro	His	Cys	Leu	Ala	Lys	Ala	Gly	Leu	Ser	Ile
65					70					75				80	

Pro	Leu	Ala	Thr	Ser	Ser	Ser	Ala	Xaa	Ile	Ile	Ser	Gly	Ala	Pro	Leu
				85					90					95	

Gly	Val	Leu	Asp	His	Val	His	Arg	Thr	Pro	Met	Gln	Lys	Ala	Ser	Ala
			100					105					110		

Arg	Thr	Gly	Pro	Ser	Phe	Leu	Ala	Arg	Arg	Phe	Glu	Met	Met	Phe	Val
	115							120				125			

Phe	Ile	Ala	Arg	Cys	Ser	Thr	Gly	Xaa	Ala	Ser	Gly	Lys	Leu	Leu	Pro
	130						135					140			

Xaa Ser Ala His Pro Trp Val Glu Cys Thr Leu Trp Asn Gly Pro Ser
 145 150 155 160
 Leu Val Pro Ser Thr Cys Glu Arg Leu Cys Pro Ser Arg His His Ala
 165 170 175
 Val Arg Ala Ala Gly Ala Gln Leu Gly Ser Arg His Arg Gly Ser Ala
 180 185 190
 Ser Met Met Thr Pro Ser Thr Trp Thr Gly Ser Thr Thr Xaa Thr Thr
 195 200 205
 Ser Leu Ser Gly Gly Ser Lys Gln Arg Ala Arg Leu Arg Ile Ser Arg
 210 215 220
 Thr Arg Ala Asn Leu Arg Trp Thr Ser Ala Ser Ile Trp Leu Gln Glu
 225 230 235 240
 Ser Lys Pro Ala Gly Ile Ser Ala Ala Arg Met Arg Arg Arg Lys Ser
 245 250 255
 Thr Ala Gln Thr Ala Ala Thr Ala Thr Val Leu Ala Ser Pro Leu Lys
 260 265 270
 Pro Tyr Leu Pro Ile Ser Gly Thr Arg Pro Arg Ser Leu Pro Arg Ala
 275 280 285
 Ser Thr Pro Thr Ala Thr Ser Pro Xaa His Ser Ser Ser Thr Pro Thr
 290 295 300
 Thr Ser Ala Glu Ala Gly Gln Asp Gln Ser Arg Arg Leu Trp Gln Xaa
 305 310 315 320
 Leu His Asn Gln Arg Xaa Ser Phe Ala Pro Gly Gln Thr Val Cys Thr
 325 330 335
 Arg Leu Thr Ser Thr Leu Arg Trp Gly Ala Val Ser Gln Thr Val Val
 340 345 350
 Phe Ala Trp Trp Thr Arg Met Arg Val Met Thr Ser Leu Xaa Trp Lys
 355 360 365
 Arg Thr Arg Leu Met Met Pro Ser Glu Asp Ser Ser Ile Ser His Xaa
 370 375 380

<210> 45

<211> 1077

<212> DNA

<213> Pseudomonas putida

<220>

<221> CDS

<222> (1) .. (1074)

<223> AAK49778

<400> 45

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acc tcc cgg ttc gat gaa ccg ctg gca ctg gcc tgt ggc cgt tca ctg	96
Thr Ser Arg Phe Asp Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu	
20 25 30	
gcc agt tac gaa ctg gtc tac gag acc tat ggc acc ctg aac gcc agc	144
Ala Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Ser	
35 40 45	
gcg agc aac gcc gtg ctg atc tgc cat gcc ctg tcc ggc cac cac cat	192
Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His	
50 55 60	
gcc gct ggc tac cat gcc gcc acc gac cgc aag ccg ggc tgg tgg gac	240
Ala Ala Gly Tyr His Ala Ala Thr Asp Arg Lys Pro Gly Trp Trp Asp	
65 70 75 80	
agc tgc atc ggc ccc gga aaa ccg atc gat acc aac cgc ttc ttc gtg	288
Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Arg Phe Phe Val	
85 90 95	
gtc agc ctg aac aac ctc ggc ggc tgc aac ggc agc acc ggc ccc agc	336
Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser	
100 105 110	
agt gtc aac cca gcc acc ggt aaa ccc tat ggc gcc gag ttc ccg gta	384
Ser Val Asn Pro Ala Thr Gly Lys Pro Tyr Gly Ala Glu Phe Pro Val	
115 120 125	
ttg acc gtg gaa gac tgg gtg cac agc cag gca cgg ctg gcc gac cgc	432
Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg	
130 135 140	
ctg ggc atc cag cag tgg gca gct atc gtc ggc ggt agc ctg ggt ggc	480
Leu Gly Ile Gln Gln Trp Ala Ala Ile Val Gly Gly Ser Leu Gly Gly	
145 150 155 160	
atg cag gcg ctg caa tgg acg atg acc tac ccc gag cgc gta cgc cac	528
Met Gln Ala Leu Gln Trp Thr Met Thr Tyr Pro Glu Arg Val Arg His	
165 170 175	
tgc gtc gac att gcc tcg gcc ccc aag ctg tcg gcg cag aac atc gcc	576
Cys Val Asp Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala	
180 185 190	
ttc aac gag gtg gcg cgt cag gcc att ctt acc gac cct gag tac cgc	624
Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Tyr Arg	
195 200 205	
aga ggc tcg ttt cca gga cca ggt gtg atc ccc aag cgc ggc ctg atg	672
Arg Gly Ser Phe Pro Gly Pro Gly Val Ile Pro Lys Arg Gly Leu Met	
210 215 220	
ctg gca cgg atg gtc ggc cac att acc tat ctg tcc gat gat tcg atg	720
Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met	
225 230 235 240	

ggt gaa aaa ttc ggc cga gag ctg aaa gcg aca agc tca act acg act 768
 Gly Glu Lys Phe Gly Arg Glu Leu Lys Ala Thr Ser Ser Thr Thr Thr
 245 250 255

tcc aca gcg tgc agt tcc agg tcg aaa gct acc tgc gct atc agg gcg 816
 Ser Thr Ala Ser Ser Ser Arg Ser Lys Ala Thr Cys Ala Ile Arg Ala
 260 265 270

agg agt ttt ccg gcc gtt tcg acg cca aca cct acc ttg atg acc aag 864
 Arg Ser Phe Pro Ala Val Ser Thr Pro Thr Pro Thr Leu Met Thr Lys
 275 280 285

gca ctg gac tat ttc gac ccg gcc gcc acg cac ggt ggt gat ctg gcc 912
 Ala Leu Asp Tyr Phe Asp Pro Ala Ala Thr His Gly Gly Asp Leu Ala
 290 295 300

gcc acc ctg gcc cac gtc acg gcg gac tac tgc atc tgt cgt tca cca 960
 Ala Thr Leu Ala His Val Thr Ala Asp Tyr Cys Ile Cys Arg Ser Pro
 305 310 315 320

ccg act gcg ctt ctc tcc ggc ccg ttc gcg cga gat cgt cga cgc gct 1008
 Pro Thr Ala Leu Leu Ser Gly Pro Phe Ala Arg Asp Arg Arg Arg Ala
 325 330 335

gat ggc cgc gcg caa gaa cgt ctg cta cct gga gat cga ttc gcc cta 1056
 Asp Gly Arg Ala Gln Glu Arg Leu Leu Pro Gly Asp Arg Phe Ala Leu
 340 345 350

cgg gca cga tgc att tcc tga 1077
 Arg Ala Arg Cys Ile Ser
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<210> 46

<211> 358

<212> PRT

<213> Pseudomonas putida

<400> 46

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Ala Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Ser
 35 40 45

Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60

Ala Ala Gly Tyr His Ala Ala Thr Asp Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80

Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Arg Phe Phe Val
 85 90 95

Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser
 100 105 110

Ser Val Asn Pro Ala Thr Gly Lys Pro Tyr Gly Ala Glu Phe Pro Val
 115 120 125
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
 130 135 140
 Leu Gly Ile Gln Gln Trp Ala Ala Ile Val Gly Gly Ser Leu Gly Gly
 145 150 155 160
 Met Gln Ala Leu Gln Trp Thr Met Thr Tyr Pro Glu Arg Val Arg His
 165 170 175
 Cys Val Asp Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Tyr Arg
 195 200 205
 Arg Gly Ser Phe Pro Gly Pro Gly Val Ile Pro Lys Arg Gly Leu Met
 210 215 220
 Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met
 225 230 235 240
 Gly Glu Lys Phe Gly Arg Glu Leu Lys Ala Thr Ser Ser Thr Thr Thr
 245 250 255
 Ser Thr Ala Ser Ser Ser Arg Ser Lys Ala Thr Cys Ala Ile Arg Ala
 260 265 270
 Arg Ser Phe Pro Ala Val Ser Thr Pro Thr Pro Thr Leu Met Thr Lys
 275 280 285
 Ala Leu Asp Tyr Phe Asp Pro Ala Ala Thr His Gly Gly Asp Leu Ala
 290 295 300
 Ala Thr Leu Ala His Val Thr Ala Asp Tyr Cys Ile Cys Arg Ser Pro
 305 310 315 320
 Pro Thr Ala Leu Leu Ser Gly Pro Phe Ala Arg Asp Arg Arg Arg Ala
 325 330 335
 Asp Gly Arg Ala Gln Glu Arg Leu Leu Pro Gly Asp Arg Phe Ala Leu
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<210> 47

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 47

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<210> 48
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 48
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<210> 49
 <211> 47
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 49
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<210> 50
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 50
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<210> 51
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 51
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<210> 52
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 52
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<210> 53
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 <212> DNA
 <213> Artificial sequence

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<223> Description of the artificial sequence:PCR primer

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<210> 54
 <211> 140
 <212> DNA
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<223> Description of the artificial sequence:PCR primer

<400> 54
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 aggcctctcg agatttaaata 140

<210> 55
 <211> 33
 <212> DNA
 <213> Artificial sequence

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<223> Description of the artificial sequence:PCR primer

<400> 55
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<210> 56
 <211> 32
 <212> DNA
 <213> Artificial sequence

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<223> Description of the artificial sequence:PCR primer

<400> 56
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<210> 57
 <211> 5091
 <212> DNA
 <213> Artificial sequence

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<223> Description of the artificial sequence:plasmid

<400> 57

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<210> 58

<211> 4323

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 58

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<210> 59

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR Primer

<400> 59

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35

<210> 60

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR Primer

<400> 60

ctctctctgt cgacgaattc aatcttacgg cctg

34

<210> 61

<211> 5860

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence:plasmid

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<210> 62

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR Primer

<400> 62

cggcaccacc gacatcatct tcacctgccc tcgttcgg

38

<210> 63

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR Primer

<400> 63

cggaacgagg gcaggtgaag atgatgtcgg tgggtgccg

38

<210> 64

<211> 1266

<212> DNA

<213> LysC mutant

<220>

<221> CDS

<222> (1)..(1266)

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Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val	
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Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys	
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Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly	
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Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn	
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1266

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<400> 65

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 <212> DNA
 <213> Artificial sequence

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<223> Description of the artificial sequence: plasmid

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 <223> Description of the artificial sequence:PCR primer

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